

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2003, 11:01:45 ; Search time 2991 Seconds

(without alignments)  
8737.653 Million cell updates/sec

Title: US-09-832-320-1

Perfect score: 898  
Sequence: 1 ctcgcacgcactcgaagctc.....aaaaaaaaaaaaaaaaaa 898

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
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20: em\_om:\*  
21: em\_or:\*  
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23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pla:\*  
35: em\_htg\_rod:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID       | Description           |
|------------|-------|-------------|--------|-------------|-----------------------|
| 1          | 329.4 | 36.7        | 144973 | 2 AC096689  | AC096689 Oryza sat    |
| 2          | 329.4 | 36.7        | 150928 | 2 AC103550  | AC103550 Oryza sat    |
| 3          | 171.6 | 19.1        | 110235 | 2 AP004057  | AP004057 Oryza sat    |
| 4          | 171.6 | 19.1        | 153428 | 2 AP005535  | AP005535 Oryza sat    |
| 5          | 140.6 | 15.7        | 716    | 8 ZMU83200  | ZMU83200 Zea mays sat |
| 6          | 134   | 14.9        | 155939 | 8 AP003853  | AP003853 Oryza sat    |
| 7          | 129   | 14.4        | 110235 | 2 AP004057  | AP004057 Oryza sat    |
| 8          | 121.8 | 13.6        | 153428 | 2 AP005535  | AP005535 Oryza sat    |
| 9          | 117.4 | 13.1        | 151673 | 8 AC097278  | AC097278 Oryza sat    |
| 10         | 113   | 12.6        | 864    | 8 AF306651  | AF306651 Oryza sat    |
| 11         | 111   | 12.4        | 129918 | 8 OSJN00280 | OSJN00280 Oryza sat   |
| 12         | 110.4 | 12.3        | 123272 | 2 AP005604  | AP005604 Oryza sat    |
| 13         | 110.4 | 12.3        | 123272 | 2 AP005309  | AP005309 Oryza sat    |
| 14         | 110.4 | 12.3        | 137275 | 2 AC128878  | AC128878 Rattus no    |
| 15         | 104.8 | 11.7        | 172838 | 2 TAET7348  | TAET7348 Trifolium    |
| 16         | 104   | 11.6        | 799    | 8 AF251277  | AF251277 Oryza sat    |
| 17         | 103.6 | 11.5        | 813    | 8 OSA278436 | OSA278436 Oryza sat   |
| 18         | 103.6 | 11.5        | 830    | 8 AP003754  | AP003754 Oryza sat    |
| 19         | 101.6 | 11.3        | 129052 | 2 AP003754  | AP003754 Oryza sat    |
| 20         | 101.2 | 11.3        | 734    | 8 HVPRIAR   | HVPRIAR Oryza sat     |
| 21         | 100.8 | 11.2        | 740    | 8 HVPRIAR   | HVPRIAR Oryza sat     |
| 22         | 99.4  | 11.1        | 582    | 8 HVPRIAR   | HVPRIAR Oryza sat     |
| 23         | 98.4  | 11.0        | 129052 | 2 AP003754  | AP003754 Oryza sat    |
| 24         | 97    | 10.8        | 784    | 8 ZMPRMS    | ZMPRMS Oryza sat      |
| 25         | 96.4  | 10.7        | 137275 | 2 AP005309  | AP005309 Oryza sat    |
| 26         | 94.6  | 10.5        | 836    | 8 AF384143  | AF384143 Trifolium    |
| 27         | 94.4  | 10.5        | 1444   | 8 HVPRIAR   | HVPRIAR Oryza sat     |
| 28         | 93.8  | 10.4        | 138467 | 2 AC111697  | AC111697 Rattus no    |
| 29         | 93.6  | 10.4        | 719    | 8 HVPRIAR   | HVPRIAR Oryza sat     |
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| 31         | 93.6  | 10.4        | 1917   | 8 HVPRIAR   | HVPRIAR Oryza sat     |
| 32         | 93.4  | 10.4        | 2031   | 8 OSU89895  | OSU89895 Oryza sat    |
| 33         | 93.4  | 10.4        | 155939 | 8 AP003853  | AP003853 Oryza sat    |
| 34         | 92.2  | 10.3        | 874    | 8 SNPRJUE9  | SNPRJUE9 Oryza sat    |
| 35         | 92.2  | 10.3        | 137785 | 2 AP005065  | AP005065 Oryza sat    |
| 36         | 92.2  | 10.3        | 176171 | 2 AP005065  | AP005065 Oryza sat    |
| 37         | 92    | 10.2        | 687    | 8 HVPRIAR   | HVPRIAR Oryza sat     |
| 38         | 91.4  | 10.2        | 108782 | 2 AC123508  | AC123508 Rattus no    |
| 39         | 91    | 10.1        | 61958  | 2 AC121467  | AC121467 Rattus no    |
| 40         | 90.6  | 10.1        | 62847  | 2 AC125560  | AC125560 Rattus no    |
| 41         | 89.6  | 10.0        | 158897 | 2 AC121439  | AC121439 Rattus no    |
| 42         | 89.6  | 10.0        | 191976 | 2 AC110411  | AC110411 Rattus no    |
| 43         | 89    | 9.9         | 136788 | 2 AC117044  | AC117044 Rattus no    |
| 44         | 88    | 9.8         | 159101 | 2 AC126205  | AC126205 Rattus no    |
| 45         | 87.8  | 9.8         | 99329  | 2 AC099247  | AC099247 Rattus no    |

# ALIGNMENTS

RESULT 1  
AC096689 144973 bp DNA linear HTG 09-JAN-2002  
Oryza sativa chromosome 3 clone OSJNB0027J18, \*\*\* SEQUENCING IN PROGRESS \*\*\*  
AC096689 6 ordered pieces.  
AC096689 3 GT-18092993  
HTG: HTGS\_PHASE2.  
SOURCE  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.  
REFERENCE  
1 (bases 1 to 144973)  
Buell,R., Hsiao,J., Zismann,V., Mofat,K.M., Hill,J.,



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* 85050 95622: contig of 10573 bp in length
* 95623 95669: gap of unknown length
* 95670 109958: contig of 14289 bp in length
* 109959 110005: gap of unknown length
* 110006 124211: contig of 14206 bp in length
* 124212 124258: gap of unknown length
* 124259 131728: contig of 7470 bp in length
* 131729 131775: gap of unknown length
* 131776 133914: contig of 2139 bp in length
* 133915 133961: gap of unknown length
* 133962 141548: contig of 7587 bp in length
* 141549 141595: gap of unknown length
* 141596 144303: contig of 2708 bp in length
* 144304 144349: gap of unknown length
* 144350 148834: contig of 4485 bp in length
* 148835 148880: gap of unknown length
* 148881 150928: contig of 2048 bp in length.

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            /cultivar="Nipponbare"
            /db_xref="taxon:4530"
            /chromosome="3"
            /clone="OSJNBa0079612"
            /note="Japanese cultivar-group"
BASE COUNT  42065 a 34725 c 33029 g 40330 t 779 others
ORIGIN
Query Match      36.7%; Score 329.4; DB 2: Length 150928;
Best Local Similarity 78.5%; Pred. No. 1,9e-32;
Matches 480; Conservative 0; Mismatches 106; Indels 17; Gaps 4;

QY 107  GCGCAATGGCGACGGGCGTGTTCCTGCGCAACCCCTCTGCGCTGCGCGCGCGCGCG
Db 68748 GCGGATGGCGCGCGCTGCTTCTGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY 167  GCGGACCCACG -GCGCGCGCTCTCATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 68691 GCGGTGCGCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
QY 226  AGCAGGTGACACCGCGACCGCGACGACGACGACGACGACGACGACGACGACGACGACG
Db 68638 AGCAGGCGAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
QY 286  ACCAGCGCGCGCGCGCGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 68578 ACCAGCGCGCGCGCGCGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY 346  CGGCGCGGCGACGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 68518 CGGCGCGGCGACGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY 400  ACCTGGGGGCGACGCCCTCTAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 68458 ACATGAGCGGAGCGCCCTTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY 460  CCGAGGTGCTGCGCTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 68398 CCGAGGTGCTGCGCTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY 520  GCGCGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 68338 GCGCGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY 580  TCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 68278 TCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY 640  CGCAGCGCAAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 68218 CGCAGCGCAAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG

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RESULT 3
AP004057/c 110235 bp DNA linear HTG 21-MAR-2002
LOCUS      Oryza sativa (japonica cultivar-group) chromosome 2 clone
DEFINITION OJ1316_E06, *** SEQUENCING IN PROGRESS ***; in ordered pieces.
ACCESSION  AP004057
VERSION     AP004057.1 GI:15208425
KEYWORDS   HTG; HTGS; PHASE2
SOURCE     Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
            clone:OJ1316_E06.
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1
            Sasaki,T., Matsumoto,T. and Yamamoto,K.,
            Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
            clone:OJ1316_E06
            Published Only in Database (2001)
REFERENCE  2 (bases 1 to 110235)
            Sasaki,T., Matsumoto,T. and Yamamoto,K.,
            Direct Submission
            Submitted (15-AUG-2001) Takuji Sasaki, National Institute of
            Agricultural Resources, Rice Genome Research Program, Kannondai
            2-1-2, Tsukuba, Ibaraki 305-8602, Japan
            (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
            Tel:81-298-38-7441, Fax:81-298-38-7468)
            The nucleotide sequence of this BAC clone was generated by
            combining Monsanto and RGP-Japan sequencing data.
            NOTE: It currently consists of 1 contigs. Gaps between the contigs
            are represented as runs of N. The order of the pieces is believed
            to be correct as given, however the sizes of the gaps between them
            are based on estimates that have provided by the submitter. This
            sequence will be replaced by the finished sequence as soon as it is
            available and the accession number will be preserved.
            * NOTE: This is a 'working draft' sequence.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.

FEATURES
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        1..110235
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            /cultivar="Nipponbare"
            /db_xref="taxon:3947"
            /chromosome="2"
            /clone="OJ1316_E06"
BASE COUNT  30404 a 23562 c 24043 g 32226 t
ORIGIN
Query Match      19.1%; Score 171.6; DB 2: Length 110235;
Best Local Similarity 59.1%; Pred. No. 8e-13;
Matches 311; Conservative 0; Mismatches 214; Indels 1; Gaps 1;

QY 147  GCGCTTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 76921 GCTCAAGGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
QY 207  GCGCGGTACCAAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGC
Db 76861 CGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY 267  GAGTACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 76802 CAGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
QY 327  AACGCGGCGCTGCTTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 76742 AGCAGGACCTGCGCGAGCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY 387  TCGGCTTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 76682 GCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG

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RESULT 12
AP005604 123272 bp DNA linear HTG 02-AUG-2002
LOCUS Oryza sativa (japonica cultivar-group) chromosome 7 clone
DEFINITION OJ1212.C12, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
ACCESSION AP005604
VERSION AP005604.1 GI:22091076
KEYWORDS HTG; HTGS-PHASE2.
SOURCE Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
        clone:OJ1212.C12.
ORGANISM Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1
AUTHORS Sasaki,T., Matsumoto,T. and Katayose,Y.
TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
        clone:OJ1212.C12
JOURNAL Published Only in Database (2002)
ACCESSION 2 (bases 1 to 123272)
VERSION AP005604
KEYWORDS Sasaki,T., Matsumoto,T. and Katayose,Y.
SOURCE Direct Submission
        Submitted (01-AUG-2002) Takuji Sasaki, National Institute of
        Agrobiological Sciences, Rice Genome Research Program, Kannondai
        2-1-2, Tsukuba, Ibaraki 305-8602, Japan
        (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
        Tel:81-298-38-7441, Fax:81-298-38-7468)
        The nucleotide sequence of this BAC clone was generated by
        combining Monsanto and RGP-Japan sequencing data.
        NOTE: It currently consists of 1 contigs. Gaps between the contigs
        are represented as runs of N. The order of the pieces is believed
        to be correct as given, however the sizes of the gaps between them
        are based on estimates that have provided by the submitter. This
        sequence will be replaced by the finished sequence as soon as it is
        available and the accession number will be preserved.
        * NOTE: This is a 'working draft' sequence.
        * This sequence will be replaced
        * by the finished sequence as soon as it is available and
        * the accession number will be preserved.
        Location/Qualifiers
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             /organism="Oryza sativa (japonica cultivar-group)"
             /cultivar="Nipponbare"
             /db_xref="taxon:39947"
             /chromosome="7"
             /clone="OJ1212.C12"
BASE COUNT 32892 a 29747 c 29268 g 31115 t 250 others
ORIGIN
Query Match 12.3%, Score 110.4; DB 2; Length 123272;
Best Local Similarity 56.6%; Pred. No. 3.1e-05;
Matches 248; Conservative 0; Mismatches 181; Indels 9; Gaps 2;

OY 251 CAACGCGAGCGGAGATACCTGGCCCGCACACAGCGCGCGGTGGGCGT 310
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 82504 CCGAGCAGCGGAGCGAGCATGTCACATCCACACAGCGCGCGGTGGGCGT 82563
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 311 GGGCCCGCTGCGGTGAGACGCGGCTTGGCGGCGCGGAGCGAGCTGGCGAGCA 370
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 82564 CCGGCGCTGTGCTGGGAGACACATCGCGGCGGTAGCGAGGCTACGCAAGCAGG 82623
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OY 371 GCGCGGAGCGGCGGTGGCGGTGGCGAGCTGGGGGCCACCCCTACGCGCGCAACA 430
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 82624 CCGCGGAGCTGGCGCTGGCGACTCGATCGACACAACTATCAGTACGCGAGACCT 82683
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 431 GGGGTGGCGAGCTACCGCGCGCCCGCCCGCAGAGTG-----GTGGCGCTGTGGGTGCG 484
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DB 82684 GTGTGGAGACCCCTCGCTCAGGCGGTGGAGCGGCGGAGCTCGCTGACCAAGTGGGTGCG 82743
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OY 485 GGAAGGGCGGTACTACACCAAGCAACAGAGTGGCGCGGCGGAGCGGTGGCGCGAC 544
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 82744 GGAGAGAGGCTCTTACGACTACGCCACAGACAGCTGGCGCGGCCCACTGTGGCGCA 82803

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OY 545 GTACACGAGTGTGTGGCGCAACACCGCGAGCTGGGTG---CGCGAGCGCAGCTG 601
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OY 662 GAGCCCTTACTAGCTACG 679
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RESULT 13
AP005604/c 123272 bp DNA linear HTG 02-AUG-2002
LOCUS Oryza sativa (japonica cultivar-group) chromosome 7 clone
DEFINITION OJ1212.C12, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
ACCESSION AP005604
VERSION AP005604.1 GI:22091076
KEYWORDS HTG; HTGS-PHASE2.
SOURCE Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
        clone:OJ1212.C12.
ORGANISM Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1
AUTHORS Sasaki,T., Matsumoto,T. and Katayose,Y.
TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
        clone:OJ1212.C12
JOURNAL Published Only in Database (2002)
ACCESSION 2 (bases 1 to 123272)
VERSION AP005604
KEYWORDS Sasaki,T., Matsumoto,T. and Katayose,Y.
SOURCE Direct Submission
        Submitted (01-AUG-2002) Takuji Sasaki, National Institute of
        Agrobiological Sciences, Rice Genome Research Program, Kannondai
        2-1-2, Tsukuba, Ibaraki 305-8602, Japan
        (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
        Tel:81-298-38-7441, Fax:81-298-38-7468)
        The nucleotide sequence of this BAC clone was generated by
        combining Monsanto and RGP-Japan sequencing data.
        NOTE: It currently consists of 1 contigs. Gaps between the contigs
        are represented as runs of N. The order of the pieces is believed
        to be correct as given, however the sizes of the gaps between them
        are based on estimates that have provided by the submitter. This
        sequence will be replaced by the finished sequence as soon as it is
        available and the accession number will be preserved.
        * NOTE: This is a 'working draft' sequence.
        * This sequence will be replaced
        * by the finished sequence as soon as it is available and
        * the accession number will be preserved.
        Location/Qualifiers
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             /cultivar="Nipponbare"
             /db_xref="taxon:39947"
             /chromosome="7"
             /clone="OJ1212.C12"
BASE COUNT 32892 a 29747 c 29268 g 31115 t 250 others
ORIGIN
Query Match 12.3%, Score 110.4; DB 2; Length 123272;
Best Local Similarity 56.6%; Pred. No. 3.1e-05;
Matches 248; Conservative 0; Mismatches 181; Indels 9; Gaps 2;

OY 251 CAACGCGAGCGGAGATACCTGGCCCGCACACAGCGCGCGGTGGGCGT 310
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 28444 CCGAGCAGCGGAGCGAGCATGTCACATCCACACAGCGCGCGGTGGGCGT 28385
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OY 311 GGGCCCGCTGCGGTGAGACGCGGCTTGGCGGCGCGGAGCGGTGGCGAGCA 370
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DB 28384 CCGGCGCTGTGCTGGGAGACACATCGCGGCGGTAGCGAGGCTACGCAAGCAGCAG 28325

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 Sodergren, E., Sonakke, T., Sparks, A., Stanley, H., Stone, R.,  
 Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,  
 Tansley, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,  
 Umanai, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q.,  
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,  
 Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K.,  
 Wu, C., Wu, Y., Wu, Y., Zhou, J., Zorrilla, S., Nelson, D.,  
 Welnscock, G., and Gibbs, R.

Direct Submission  
 Unpublished  
 2 (bases 1 to 172838)  
 Worley, K.C.  
 Direct Submission  
 Submitted (24-JUL-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 172838)  
 Worley, K.C.  
 Direct Submission  
 Submitted (02-AUG-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Aug 1, 2002 this sequence version replaced gi:21951102.

----- Genome Center -----  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information -----  
 Center project name: KAXI  
 Center clone name: CH230-51P16  
 ----- Summary Statistics -----  
 Sequencing vector: Plasmid  
 Chemistry: Dye-terminator Big Dye 100% of reads  
 Assembly program: Phrap, version 0.990329  
 Consensus quality: 117263 bases at least Q40  
 Consensus quality: 122934 bases at least Q30  
 Consensus quality: 128074 bases at least Q20

\* NOTE: Estimated insert size may differ from sequence length  
 \* (see <http://www.hgsc.bcm.tmc.edu/docs/Genbankdraftdata.html>).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 55 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

|       |        |                             |
|-------|--------|-----------------------------|
| 1     | 1127:  | contig of 1127 bp in length |
| 1128  | 1227:  | gap of unknown length       |
| 1228  | 2910:  | contig of 1683 bp in length |
| 2911  | 3010:  | gap of unknown length       |
| 3011  | 4361:  | contig of 1351 bp in length |
| 4362  | 4461:  | gap of unknown length       |
| 4462  | 5971:  | contig of 1510 bp in length |
| 5972  | 6071:  | gap of unknown length       |
| 6072  | 7285:  | contig of 1214 bp in length |
| 7286  | 7385:  | gap of unknown length       |
| 7386  | 8693:  | contig of 1308 bp in length |
| 8694  | 8793:  | gap of unknown length       |
| 8794  | 10216: | contig of 1423 bp in length |
| 10217 | 10316: | gap of unknown length       |

|       |        |                             |
|-------|--------|-----------------------------|
| 10317 | 12126: | contig of 1810 bp in length |
| 12127 | 12226: | gap of unknown length       |
| 12227 | 13410: | contig of 1184 bp in length |
| 13411 | 13510: | gap of unknown length       |
| 13511 | 15382: | contig of 1872 bp in length |
| 15383 | 15482: | gap of unknown length       |
| 15483 | 17296: | contig of 1814 bp in length |
| 17297 | 17395: | gap of unknown length       |
| 17397 | 18901: | contig of 1505 bp in length |
| 18902 | 19001: | gap of unknown length       |
| 19002 | 20176: | contig of 1175 bp in length |
| 20177 | 20276: | gap of unknown length       |
| 20277 | 21310: | contig of 1034 bp in length |
| 21311 | 21410: | gap of unknown length       |
| 21411 | 22705: | contig of 1295 bp in length |
| 22706 | 22805: | gap of unknown length       |
| 22806 | 24404: | contig of 1599 bp in length |
| 24405 | 24504: | gap of unknown length       |
| 24505 | 26132: | contig of 1628 bp in length |
| 26133 | 28232: | gap of unknown length       |
| 28233 | 28257: | contig of 2025 bp in length |
| 28258 | 28357: | gap of unknown length       |
| 28358 | 30252: | contig of 1895 bp in length |
| 30253 | 30352: | gap of unknown length       |
| 30353 | 31812: | contig of 1460 bp in length |
| 31813 | 31912: | gap of unknown length       |
| 31913 | 33873: | contig of 1961 bp in length |
| 33874 | 33973: | gap of unknown length       |
| 33974 | 37205: | contig of 3232 bp in length |
| 37206 | 37305: | gap of unknown length       |
| 37306 | 39711: | contig of 2406 bp in length |
| 39712 | 39811: | gap of unknown length       |
| 39812 | 42028: | contig of 2217 bp in length |
| 42029 | 42128: | gap of unknown length       |
| 42129 | 43600: | contig of 1472 bp in length |
| 43601 | 43700: | gap of unknown length       |
| 43701 | 46797: | contig of 3097 bp in length |
| 46798 | 46897: | gap of unknown length       |
| 46898 | 49143: | contig of 2246 bp in length |
| 49144 | 49243: | gap of unknown length       |
| 49244 | 50897: | contig of 1654 bp in length |
| 50898 | 50997: | gap of unknown length       |
| 50999 | 53047: | contig of 2050 bp in length |
| 53048 | 53147: | gap of unknown length       |
| 53148 | 55878: | contig of 2731 bp in length |
| 55879 | 55978: | gap of unknown length       |
| 55979 | 58722: | contig of 2744 bp in length |
| 58723 | 58822: | gap of unknown length       |
| 58823 | 60365: | contig of 1543 bp in length |
| 60366 | 60465: | gap of unknown length       |
| 60466 | 63255: | contig of 2794 bp in length |
| 63260 | 63359: | gap of unknown length       |
| 63360 | 65994: | contig of 2633 bp in length |
| 65995 | 66094: | gap of unknown length       |
| 66095 | 69757: | contig of 3663 bp in length |
| 69758 | 69857: | gap of unknown length       |
| 69858 | 72521: | contig of 2664 bp in length |
| 72522 | 72621: | gap of unknown length       |
| 72622 | 74779: | contig of 2158 bp in length |
| 74780 | 74892: | gap of unknown length       |
| 74880 | 78892: | contig of 4013 bp in length |
| 78893 | 78992: | gap of unknown length       |
| 78993 | 83087: | contig of 4095 bp in length |
| 83088 | 83187: | gap of unknown length       |
| 83188 | 87020: | contig of 3833 bp in length |
| 87021 | 87120: | gap of unknown length       |
| 87121 | 90872: | contig of 3752 bp in length |
| 90873 | 90972: | gap of unknown length       |
| 90973 | 93397: | contig of 2425 bp in length |
| 93398 | 93497: | gap of unknown length       |
| 93498 | 95391: | contig of 1894 bp in length |
| 95392 | 95491: | gap of unknown length       |
| 95492 | 98921: | contig of 3430 bp in length |

\* 98922 99021: gap of unknown length  
\* 99022 104293: contig of 5272 bp in length  
\* 104294 104394: gap of unknown length  
\* 104394 108459: contig of 4066 bp in length  
\* 108459 108559: gap of unknown length  
\* 108559 108560: gap of unknown length  
\* 113545 113545: contig of 4986 bp in length  
\* 113546 113645: gap of unknown length  
\* 113646 117970: contig of 4325 bp in length  
\* 117971 118070: gap of unknown length  
\* 118071 122690: contig of 4620 bp in length  
\* 122691 122790: gap of unknown length  
\* 122791 127623: contig of 4833 bp in length  
\* 127624 127723: gap of unknown length  
\* 127724 136739: contig of 9016 bp in length  
\* 136740 136839: gap of unknown length  
\* 136840 142131: contig of 5292 bp in length  
\* 142132 142231: gap of unknown length  
\* 142232 150986: contig of 8755 bp in length  
\* 150987 151086: gap of unknown length  
\* 151087 160415: contig of 9329 bp in length

## Query Match

Best Local Similarity 11.7%; Score 104.8; DB 2; Length 172838;  
Pred. No. 0.00015;  
Matches 220; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

QY 102 CCCGCGCCATGCGCCACGCGCTGTCTCTCCGCACTCTCCGCGCTGTGCGCGCG 161  
Db 24026 CCGGCGCCCGGCGCCCGCGCCCGCGCCCGCGCCCGCGCCCGCGCGCGCGCG 23967  
QY 162 CCGGCGCCCGACCCACGCGCGCGCGCTCTCTATGCGGCGCGCGCGCGCGCGCG 221  
Db 23966 CCGGCGCCCGGCG 23907  
QY 222 GCGCAGCAGGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 281  
Db 23906 GCGGCG 23847  
QY 282 CACAMACAGGCGCGCGCGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 341  
Db 23846 CCGGCG 23787  
QY 342 TCGGCG 401  
Db 23786 GAGGCG 23727  
QY 402 GTGGGCG 461  
Db 23726 GGGGCG 23667  
QY 462 GAGGTGTGCG 521  
Db 23666 GGGGCG 23607  
QY 522 GCCGCGCGCG 530  
Db 23606 GGGGAGGGG 23598

Search completed: March 18, 2003, 15:14:28  
Job time : 3824 secs

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 19, 2003, 09:35:37 ; Search time 18 Seconds  
(without alignments)  
1084.183 Million cell updates/sec

Title: US-09-832-320-2

Perfect score: 1085

Sequence: 1 MAHSRSHHLLLPAPMATA.....ATLTCLYNPHGNVQGSPPY 203

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR\_73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 357.5 | 32.9        | 214    | 2     | S65052      |
| 2          | 331   | 30.5        | 163    | 2     | T02054      |
| 3          | 318   | 29.3        | 140    | 2     | A33155      |
| 4          | 308.5 | 28.4        | 164    | 2     | S37166      |
| 5          | 307.5 | 28.3        | 172    | 2     | T04990      |
| 6          | 304   | 28.0        | 167    | 2     | S14969      |
| 7          | 304   | 28.0        | 167    | 2     | B24620      |
| 8          | 304   | 28.0        | 184    | 2     | S10205      |
| 9          | 302.5 | 27.9        | 179    | 2     | S22531      |
| 10         | 297.5 | 27.4        | 163    | 2     | T04989      |
| 11         | 296   | 27.3        | 168    | 2     | C24620      |
| 12         | 294   | 27.1        | 166    | 2     | S71270      |
| 13         | 290.5 | 26.8        | 164    | 2     | S52627      |
| 14         | 288.5 | 26.6        | 164    | 2     | S39474      |
| 15         | 288   | 26.5        | 161    | 2     | T01693      |
| 16         | 288   | 26.5        | 162    | 2     | T08154      |
| 17         | 288   | 26.5        | 162    | 2     | D86143      |
| 18         | 286   | 26.4        | 168    | 2     | A24620      |
| 19         | 285.5 | 26.3        | 164    | 2     | S52626      |
| 20         | 285   | 26.3        | 205    | 2     | T48294      |
| 21         | 284   | 26.2        | 168    | 2     | T07330      |
| 22         | 283.5 | 26.1        | 167    | 2     | S51679      |
| 23         | 281.5 | 25.9        | 159    | 2     | S26238      |
| 24         | 277.5 | 25.6        | 159    | 1     | VCT014      |
| 25         | 271   | 25.0        | 185    | 2     | T10677      |
| 26         | 269   | 24.8        | 190    | 2     | T04232      |
| 27         | 268.5 | 24.7        | 173    | 2     | S47171      |
| 28         | 265.5 | 24.5        | 161    | 2     | H84518      |
| 29         | 263.5 | 24.3        | 161    | 2     | S65777      |

|    |       |      |     |   |        |                     |
|----|-------|------|-----|---|--------|---------------------|
| 30 | 261.5 | 24.1 | 174 | 2 | S71554 | pathogenesis-relat  |
| 31 | 260.5 | 24.0 | 164 | 2 | T04299 | pathogenesis-relat  |
| 32 | 260   | 24.0 | 177 | 2 | S04728 | pathogenesis-relat  |
| 33 | 257.5 | 23.7 | 175 | 2 | S43894 | pathogenesis-relat  |
| 34 | 257   | 23.7 | 161 | 2 | E85354 | PR-1-like protein   |
| 35 | 256.5 | 23.6 | 210 | 2 | T04233 | pathogenesis-relat  |
| 36 | 249.5 | 23.0 | 161 | 2 | T52399 | pathogenesis-relat  |
| 37 | 246   | 22.7 | 176 | 2 | F84583 | pathogenesis-relat  |
| 38 | 243   | 22.4 | 161 | 2 | B96537 | pathogenesis-relat  |
| 39 | 242   | 22.3 | 168 | 2 | T07146 | hypothetical prote  |
| 40 | 242   | 22.3 | 177 | 2 | T08126 | pathogenesis-relat  |
| 41 | 234   | 21.6 | 162 | 2 | A96537 | pathogenesis-relat  |
| 42 | 197   | 18.2 | 160 | 2 | D85077 | hypothetical prote  |
| 43 | 191.5 | 17.6 | 177 | 2 | D84583 | probable pathogene  |
| 44 | 171.5 | 15.8 | 81  | 2 | A05264 | probable pathogene  |
| 45 | 167   | 15.4 | 204 | 2 | S27448 | Sc7 protein - bracc |

#### ALIGNMENTS

##### RESULT 1

PISTILL-Specific protein stsl4 precursor - potato

C:Species: Solanum tuberosum (potato)

C>Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 20-Jun-2000

C:Accession: S65052

R:van Eldik, G.J.; Wingen, M.; Rulter, R.K.; van Herpen, M.M.A.; Schrauwen, J.A.M.; Plant Mol. Biol. 30, 171-176, 1996

A:Title: Molecular analysis of a pistill-specific gene expressed in the stigma and sty

A:Reference number: S65052; MID:96197407; PMID:8616234

A:Accession: S65052

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-214 <V>AN>

A:Cross-references: EMBL:X82652; NID:g1236784; PIDN:CA457976.1; PID:g1236785

C:Genetics:

A:Gene: stsl4

C:Superfamily: pathogenesis-related leaf protein

Query Match 32.9%; Score 357.5; DB 2; Length 214;  
Best Local Similarity 41.3%; Pred. No. 7.8e-22;  
Matches 76; Conservative 26; Mismatches 75; Indels 7; Gaps 3;

|    |     |   |     |
|----|-----|---|-----|
| QY | 22  | LILATLILACAAAPPHGARVLMPCAGAVTKAQCQGTSGSNATDEXLAPHQAARAV     | 81  |
| DB | 36  | LLEFQFLTLTASTLTHISAQTVPPPPPTSA-----ATPPSRAOEFLDAHNRARSEV    | 90  |
| QY | 82  | GVAPLIRNAGLASAAAGTVAQORROGCAFDVGAAPYGANQGMASR-ARPAEVALMV    | 140 |
| DB | 91  | GVGPTLWSPMLAKETSLVARYQDKONCSFANLSNCKTGGQJMASGTVTPRMAVDSWV   | 150 |
| QY | 141 | AESRYTYTHANNITCAAGRCQGTYYQVVMRTAEVCAQASCATG-ATLTCLYNPHGNVQG | 199 |
| DB | 151 | AEKKFYENNSCTGDKCGVYQIWMKKSIELGCAQPRCYECPATLVTCFPPGNTVIG     | 210 |
| QY | 200 | OSPPY 203   |     |
| DB | 211 | EKPY 214  |     |

##### RESULT 2

T02054 pathogenesis related protein-1 - maize

C:Species: Zea mays (maize)

C>Date: 26-Feb-1999 #sequence\_revision 26-Feb-1999 #text\_change 11-May-2000

C:Accession: T02054

R:Morris, S.W.; Vernooij, B.; Titartarn, S.; Starrett, M.; Thomas, S.; Willse, C.C.; F

Mol. Plant Microbe Interact. 11, 643-658, 1998

A:Title: Induced resistance responses in maize.

A:Reference number: Z14524; MID:98513983; PMID:9650297

A:Accession: T02054

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
A:Residues: 1-163 <MOR>  
A:Cross-references: EMBL:U82200; NID:g3290003; PIDD:AAAC25629.1; PTD:g3290004  
C:Genetics:  
C:Gene: PR-1  
C:Superfamily: pathogenesis-related leaf protein

|                       |        |                    |        |                |
|-----------------------|--------|--------------------|--------|----------------|
| Query Match           | 30.5%; | Score 331;         | DB 2;  | Length 163;    |
| Best Local Similarity | 39.0%; | Pred. No. 8.3e-20; |        |                |
| Matches               | 73;    | Conservative       | 21;    | Mismatches 61; |
|                       |        |                    | Indels | 32;            |
|                       |        |                    | Gaps   | 6;             |

|    |     |  |     |
|----|-----|--|-----|
| QY | 20  | ACLLATLTLACAPAPPHGGRVILMPGAGAVTKRAQGGGSSNNATADLEYIAHPHQAA          | 79  |
|    |     | : : |     |
| Db | 6   | ACLLAAMAAALVAPC-----TQNSPQD-YDPHNHARA                              | 39  |
| QY | 80  | AVGAPFLMNNGIASAAAGIYAQQRGGCGAFADYGASPYGAGNAGSYRA--RPAPYA           | 137 |
|    |     | :   |     |
| Db | 40  | DVGAPVSMDDTVAYIAQSYAQAQ--KQDCKLIHSG-GPIGEMLPFGSAGADMSSADAVG        | 96  |
| QY | 138 | LMVAEGRIYTHANNTCAGAGRCGTYTVYMRNRAEVCQAQASCATGA-TITLCLYHPGN         | 196 |
|    |     | :   |     |
| Db | 97  | SWVSKRQYVHDHDTSCSAGQVCGHYTVYMDSTALICAGVYCDNNAQVITISYPPEN           | 156 |

|    |     |         |     |
|----|-----|---------|-----|
| QY | 197 | VQGQSPY | 203 |
|    |     | 11:111  |     |
| Db | 157 | VVGESPY | 163 |

### RESULT 3

A:33155 pathogenesis-related protein 1 - maize  
C:Species: Zea mays (maize)  
C:Date: 08-Mar-1991 #sequence\_revision 08-Mar-1991 #text\_change 31-Dec-1993  
C:Accession: A33155  
R:Gillikin, J.; Burkhart, W.; Graham, J.S.  
submitted to the Protein Sequence Database, February 1991  
A:Reference number: A33155  
A:Accession: A33155  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-140 <GIL>  
C:Superfamily: pathogenesis-related leaf protein

Query Match 29.3%; Score 318; DB 2; Length 140;  
Best Local Similarity 46.4%; Pred. No. 8.1e-19;  
Matches 64; Conservative 18; Mismatches 50; Indels 6; Gaps 4;

[illegible]

## RESULT 4

pathogenesis-related protein 1a - barley  
N:Alternate names: pathogenesis-related protein Hv-1a  
C:Species: Hordeum vulgare (barley)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Aug-1999  
C:Accession: S37166  
R:Bryggelsson, T., Sommer-Knudsen, J., Grgerssen, P.L., Collinge, D.B., Ek, B., Thordal  
submitted to the EMBL Data Library, September 1993  
A:Description: Purification characterization and molecular cloning of basic PR-1-type pa  
A:Reference number: S37166  
A:Accession: S37166  
A:Status: preliminary

A: Molecule type: mRNA  
 A: Residues: 1-164 <BRI>  
 A: Cross-references: EMBL: X74939; NID: g401830; PIDN: CAA52893.1; PID: g401831  
 C: Superfamily: pathogenesis-related leaf protein

|                       |        |                    |       |                |
|-----------------------|--------|--------------------|-------|----------------|
| Query Match           | 28.4%  | Score 308.5;       | DB 2; | Length 164;    |
| Best Local Similarity | 41.0%; | Pred. No. 5.5e-18; |       |                |
| Matches               | 75;    | Conservative       | 19;   | Mismatches 62; |
|                       |        |                    |       | Indels 27;     |
|                       |        |                    |       | Gaps 7;        |

[illegible]

|    |     |     |     |
|----|-----|-----|-----|
| QY | 201 | SPY | 203 |
|    |     | 11  |     |
| Db | 162 | KPY | 164 |

## RESULT 5

pathogenesis-related protein T16L1.220 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 23-Apr-1999 #sequence 23-Apr-1999 #text\_change 11-Jun-1999  
C:Accession: T04990  
R:Byers, M.; Obermayer, B.; Deuschénbauer, S.; Piravandi, E.; Hohelsel, J.; Mewes, H.  
submitted to the Protein Sequence Database, November 1998  
A:Reference number: Z15393  
A:Accession: T04990  
A:Molecule type: DNA  
A:Residues: 1-172 <BEV>  
A:Cross-references: EMBL:AL01394  
A:Experimental source: cultivar Columbia; BAC clone T16L1  
C:Genetics:  
A:Map position: 4  
A:Note: T16L1.220  
C:Superfamily: pathogenesis-related leaf protein

|                       |        |                    |        |                |
|-----------------------|--------|--------------------|--------|----------------|
| Query Match           | 28.3%; | Score 307.5;       | DB 2;  | Length 172;    |
| Best Local Similarity | 44.7%; | Pred. No. 6.9e-18; |        |                |
| Matches               | 63;    | Conservative       | 19;    | Mismatches 56; |
|                       |        |                    | Indels | 3;             |
|                       |        |                    | Gaps   | 3;             |

[illegible]

## RESULT

pathogenesis-related protein - maize  
C.Species: Zea mays (maize)  
C.Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Aug-1999  
C.Accession: S14969  
R:Casacuberta, J.M.; Puigdomenech, P.; San Segundo, B.  
Plant Mol. Biol. 16: 527-536,1991  
A:Title: A gene coding for a basic pathogenesis-related (PR-like) protein from Zea mays  
A:Reference number: S14969; MUID:91329688; PMID:1714315  
A:Accession: S14969







QY 162 YTOVWBNTEAYGCAASCATGATITLCLYNPHGNVQOSPY 203  
| | | | | : : | | : | | : | | : | |  
Db 120 YTOVWNRKSVRLGCAKVRONNGTIIISCNIDPRGNVYNEKPY 161

Search completed: March 19, 2003, 09:36:05  
Job time : 19 secs



GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 19, 2003, 09:35:38 ; Search time 11 Seconds  
(without alignments)

765.427 Million cell updates/sec

Title: US-09-832-320-2

Perfect score: 1085

Sequence: 1 MAHSSRHHLLLPAPMATA.....ATLTLCLYNPHGVQGSQSPY 203

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SWISSPROT\_40.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID          | Description         |
|------------|-------|-------------|--------|-------------|---------------------|
| 1          | 357.5 | 32.9        | 214    | ST14_SOLTU  | Q41495 solanum tub  |
| 2          | 304   | 28.0        | 167    | PRMS_MAIZE  | Q00008 zea mays (m  |
| 3          | 304   | 28.0        | 168    | PR1B_TOBAC  | P07053 nicotiana t  |
| 4          | 296   | 27.3        | 168    | PR1C_TOBAC  | P05042 nicotiana t  |
| 5          | 290.5 | 26.8        | 164    | PR12_HORVU  | P35792 hordeum vul  |
| 6          | 288.5 | 26.6        | 164    | PR1_HORVU   | P05968 hordeum vul  |
| 7          | 288   | 26.5        | 161    | PR1_ARATH   | P33154 arabidopsis  |
| 8          | 286   | 26.4        | 168    | PR1A_TOBAC  | P08299 nicotiana t  |
| 9          | 285.5 | 26.3        | 164    | PR13_HORVU  | P35793 hordeum vul  |
| 10         | 281.5 | 25.9        | 167    | PR1_SAMNI   | Q41359 sambucus ni  |
| 11         | 281.5 | 25.9        | 159    | PR04_LYCES  | Q04108 lycopersico  |
| 12         | 277.5 | 25.6        | 173    | PR06_LYCES  | P04284 lycopersico  |
| 13         | 268.5 | 24.7        | 173    | PR1_MEPTR   | Q40374 medicago tr  |
| 14         | 260   | 24.0        | 177    | PR1L_TOBAC  | P11670 nicotiana t  |
| 15         | 257.5 | 23.7        | 175    | PR1A_LYCES  | Q08697 lycopersico  |
| 16         | 167   | 13.4        | 204    | SC7_SCHCO   | P35794 schizophyll  |
| 17         | 166.5 | 15.3        | 214    | SC14_SCHCO  | P35795 schizophyll  |
| 18         | 163   | 15.0        | 881    | YJH8_YEAST  | P47033 saccharomyc  |
| 19         | 161   | 14.8        | 299    | YJH9_YEAST  | P47032 saccharomyc  |
| 20         | 129   | 11.9        | 329    | KX23_YEAST  | P36110 saccharomyc  |
| 21         | 127.5 | 11.8        | 206    | VAS_VESFL   | P35787 vesputia vid |
| 22         | 125.5 | 11.6        | 244    | ABE1_MOUSE  | Q05401 mus musculu  |
| 23         | 125.5 | 11.6        | 312    | YR81_CAEEL  | Q05566 caenorabdi   |
| 24         | 124.5 | 11.5        | 234    | VAS_SOLIN   | P35785 vesputia pen |
| 25         | 123   | 11.3        | 204    | VAS_VESPE   | P35788 vesputia fla |
| 26         | 121   | 11.2        | 204    | VAS_VESFL   | P35789 vesputia fla |
| 27         | 120   | 11.1        | 245    | CRS3_HORSE  | O15010 equus cabal  |
| 28         | 119.5 | 11.0        | 205    | VAS_POLEX   | P35759 polistes ex  |
| 29         | 118.5 | 10.9        | 203    | VAS_POLEX   | P35758 polistes ex  |
| 30         | 117.5 | 10.8        | 209    | VAS_POLAN   | Q05109 polistes an  |
| 31         | 117.5 | 10.7        | 424    | VAS_ANCCA   | Q16937 ancylostoma  |
| 32         | 116.5 | 10.7        | 215    | VAS3_DOLMA  | P10737 dolichovesp  |
| 33         | 116   | 10.7        | 242    | HELO_HELIHO | Q91055 heloderma h  |

|    |       |      |     |   |            |                     |
|----|-------|------|-----|---|------------|---------------------|
| 34 | 115   | 10.6 | 202 | 1 | VAS_VESMA  | P81657 vespa manda  |
| 35 | 114.5 | 10.6 | 676 | 1 | ICP0_HSVBU | P29128 bovine herp  |
| 36 | 113.5 | 10.5 | 246 | 1 | ABG_RAT    | P12020 rattus norv  |
| 37 | 113   | 10.4 | 204 | 1 | VAS_VESGE  | P35784 vesputia ger |
| 38 | 112   | 10.3 | 211 | 1 | VAS_SOLTU  | P35779 solenopsis   |
| 39 | 112   | 10.3 | 227 | 1 | VAS_VESVO  | Q05110 vesputia vul |
| 40 | 111   | 10.2 | 227 | 1 | VAS2_DOLMA | P10736 dolichovesp  |
| 41 | 110.5 | 10.2 | 442 | 1 | GAT4_HUMAN | P43694 homo sapien  |
| 42 | 110   | 10.1 | 183 | 1 | CRVP_TRIMU | P79845 trimeresuru  |
| 43 | 110   | 10.1 | 204 | 1 | VAS_VESMC  | P35760 vesputia mac |
| 44 | 107.5 | 9.9  | 206 | 1 | VAS_POLDO  | P81656 polistes do  |
| 45 | 105.5 | 9.7  | 205 | 1 | VAS_VESSO  | P35786 vesputia squ |

## ALIGNMENTS

| RESULT 1 | ST14_SOLTU   | STANDARD: | PRT:      | 214 AA.                          |
|----------|--|-----------|-----------|----------------------------------|
| ID       | ST14_SOLTU   |           |           |                                  |
| AC       | Q41495;  |           |           |                                  |
| DT       | 01-NOV-1997 (Rel. 35, Created)   |           |           |                                  |
| DT       | 01-NOV-1997 (Rel. 35, Last sequence update)  |           |           |                                  |
| DT       | 01-NOV-1997 (Rel. 35, Last annotation update)  |           |           |                                  |
| DE       | SRS14 protein precursor.   |           |           |                                  |
| GN       | SRS14.   |           |           |                                  |
| OS       | Solanum tuberosum (Potato).  |           |           |                                  |
| OC       | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;   |           |           |                                  |
| OC       | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;   |           |           |                                  |
| OC       | Asteridae; euasterids I; Solanales; Solanaceae; Solanum.   |           |           |                                  |
| OX       | NCBI_TaxID=4113;   |           |           |                                  |
| RN       | [1]  |           |           |                                  |
| RP       | SEQUENCE FROM N.A.   |           |           |                                  |
| RC       | STRAIN=cv. Datura; TISSUE=stigma;  |           |           |                                  |
| EX       | MEDLINE=96197407; PubMed=8616234;  |           |           |                                  |
| RA       | van Eldik G.J., Wiggins M., Rutter R.K., van Herpen M.M.A.,  |           |           |                                  |
| RA       | Schrauwen J.A.M., Willems G.J.;  |           |           |                                  |
| RT       | "Molecular analysis of a pistil-specific gene expressed in the stigma  |           |           |                                  |
| RT       | and cortex of Solanum tuberosum.";   |           |           |                                  |
| RI       | Plant Mol. Biol. 30:171-176(1996)  |           |           |                                  |
| RL       |  |           |           |                                  |
| CC       | - FUNCTION: MAY PROTECT THE OUTER TISSUES OF THE PISTIL FROM   |           |           |                                  |
| CC       | PATHOGEN ATTACK.   |           |           |                                  |
| CC       | - TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE STIGMA AND STYLAR  |           |           |                                  |
| CC       | CORTEX THROUGHOUT PISTIL DEVELOPMENT. NOT EXPRESSED IN OTHER   |           |           |                                  |
| CC       | ORGANS.  |           |           |                                  |
| CC       | - DEVELOPMENTAL STAGE: ACCUMULATES IN THE PISTIL AROUND 120 HOURS  |           |           |                                  |
| CC       | BEFORE ANTHESIS AND INCREASES TOWARDS THE END OF FLOWER  |           |           |                                  |
| CC       | DEVELOPMENT, WITH A MAXIMUM AT ANTHESIS.   |           |           |                                  |
| CC       | - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPXL;  |           |           |                                  |
| CC       | INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.   |           |           |                                  |
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| CC       | -----  |           |           |                                  |
| CC       | EMBL: X82652; CAA57976.1; -  |           |           |                                  |
| CC       | HSSP: P04284; 1CFE.  |           |           |                                  |
| CC       | InterPro: IPR001283; Allrgn_V5/TPXL.   |           |           |                                  |
| CC       | Pfam: PF00188; SCP_1.  |           |           |                                  |
| CC       | ProDom: PD000542; Allrgn_V5/TPXL; 1.   |           |           |                                  |
| CC       | SMART: SM00198; SCP_1.   |           |           |                                  |
| CC       | PROSITE: PS01009; SCP_AGS_PRL_SCP_1; FALSE_NEG.  |           |           |                                  |
| CC       | DR POSITIVE: PS01010; SCP_AGS_PRL_SCP_2; FALSE_NEG.  |           |           |                                  |
| CC       | Repeat: Signal.  |           |           |                                  |
| CC       | FT SIGNAL  | 1         | 19        | POTENTIAL.                       |
| CC       | FT CHAIN   | 20        | 214       | SRS14 PROTEIN.                   |
| CC       | FT REPEAT  | 13        | 19        | 3.5 X 2 AA TANDEM REPEAT OF Y-I. |
| CC       | FT DOMAIN  | 59        | 65        | POLY-PRO.                        |
| CC       | FT SEQUENCE  | 214 AA;   | 23887 MW; | 6CC7919DE2C3C2EF CRC64;          |



```

CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
CC AGAINST PATHOGENS.
CC -1- SUBCELLULAR LOCATION: ACCUMULATE IN WITHIN THE VACUOLES OF
CC SPECIALIZED CELLS KNOWN AS CRYSTAL IDIOBLASTS.
CC -1- INDUCTION: SYNTHESIZED DURING PATHOGEN INFECTION OR OTHER STRESS-
CC RELATED RESPONSES.
CC -1- PTM: THREE DISULFIDE BONDS ARE PRESENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
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CC -----
DR EMBL; D90197; BAA14221.1; -
DR EMBL; X03465; CAA27183.1; -
DR EMBL; X12486; CAA31009.1; -
DR EMBL; X17680; CAA35665.1; -
DR PIR; B24620; B24620.
DR PIR; S07579; S07579.
DR HSSP; P04284; ICFE.
DR InterPro; IPR001283; Allrgn_V5/7px1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPXLIKE.
DR ProDom; PD000542; Allrgn_V5/7px1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; SCP AG5_PRL_SG7_1; 1.
DR PROSITE; PS01010; SCP AG5_PRL_SG7_2; 1.
KW Plant defense; Pathogenesis-related protein; Multigene family; Signal.
FT SIGNAL 1 30
FT CHAIN 31 168
FT CONFLICT 16 16 S -> A (IN REF. 3).
FT SEQUENCE 168 AA; 18499 MW; 61FCE3B87A7F1F1 CRC64;
SQ
Query Match 28.0%; Score 304; DB 1; Length 168;
Best Local Similarity 44.3%; Pred. No. 2, 3e-17;
Matches 66; Conservative 17; Mismatches 52; Indels 14; Gaps 4;
QY 61 SCSNMTADLEYLAPHNQARAANGVAPLRNMGASAAAGTYAQQRRGGCAFPADVGA---- 116
DB 28 SRAQNSQDDYDIAHNTARADVGEPLTWDDQVAAAYAAQNTYSQ-----LAADCNLVHSH 80
QY 117 SPYGAN--QGMASYRARAPEVVALMVAEGRYTHANNTCAGRCQCTYTQVWRRNTAEVG 174
DB 81 GGYENLQAGSGDEMT-AAKAVEMWVDEKQYDHDSTCAQGVGCHYTQVWRRNSVRVG 139
QY 175 CAQASCATGATLTLCLYPHGNGVGGSEPY 203
DB 140 CARVKNCGVYVSCNDPDPGNVIGOSPY 168
DB
RESULT 4
PRIC.TOBAC STANDARD; PRT; 168 AA.
AC P09042;
DR 01-NOV-1988 (Rel. 09, Created)
DR 01-APR-1990 (Rel. 14, Last sequence update)
DR 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pathogenesis-related protein 1C precursor (Pr-1C).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; eusterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Samsun NN; Tissue=leaf;
RX MEDLINE=90174915; PubMed=2308825;
RA Ohshima M., Harada N., Matsuo M., Ohashi Y.;

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RT "The nucleotide sequence of pathogenesis-related (PR) 1c protein gene
RT of tobacco.";
RT Nucleic Acids Res. 18:182-182(1990).
RN [2]
RP SEQUENCE OF 6-168 FROM N.A.
RC STRAIN=cv. Xanthi;
RX MEDLINE=89041576; PubMed=3166451;
RA Cuth J.R., Dixon D.D., Carr J.P., Klessig D.F.;
RT "Isolation and nucleotide sequence of cDNA clones for the
RT pathogenesis-related proteins PRL1, PRLb and PR1c of Nicotiana
RT tabacum cv. Xanthi not induced by TMV infection.";
RT Nucleic Acids Res. 16:9861-9861(1988).
RN [3]
RP SEQUENCE OF 8-168 FROM N.A.
RC STRAIN=cv. Samsun NN;
RX MEDLINE=87231027; PubMed=3295779;
RA Pflizner U.M., Goodman H.M.;
RT "Isolation and characterization of cDNA clones encoding pathogenesis-
RT related proteins from tobacco mosaic virus infected tobacco plants.";
RT Nucleic Acids Res. 15:4449-4449(1987).
RN [4]
RP SUBCELLULAR LOCATION.
RX MEDLINE=91224081; PubMed=2026137;
RA Dixon D.C., Cuth J.R., Klessig D.F.;
RT "Differential targeting of the tobacco PR-1 pathogenesis-related
RT proteins to the extracellular space and vacuoles of crystal
RT idioblasts.";
RT EMBL J. 10:1317-1324(1991).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
CC AGAINST PATHOGENS.
CC -1- SUBCELLULAR LOCATION: ACCUMULATE IN WITHIN THE VACUOLES OF
CC SPECIALIZED CELLS KNOWN AS CRYSTAL IDIOBLASTS.
CC -1- INDUCTION: SYNTHESIZED DURING PATHOGEN INFECTION OR OTHER STRESS-
CC RELATED RESPONSES.
CC -1- PTM: THREE DISULFIDE BONDS ARE PRESENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
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CC -----
DR EMBL; X17681; CAA35666.1; -
DR EMBL; X05454; CAA29023.1; -
DR EMBL; X12487; CAA31010.1; -
DR PIR; S07580; S07580.
DR HSSP; P04284; ICFE.
DR InterPro; IPR001283; Allrgn_V5/7px1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPXLIKE.
DR ProDom; PD000542; Allrgn_V5/7px1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; SCP AG5_PRL_SG7_1; 1.
DR PROSITE; PS01010; SCP AG5_PRL_SG7_2; 1.
KW Plant defense; Pathogenesis-related protein; Multigene family; Signal.
FT SIGNAL 1 30
FT CHAIN 31 168
FT SEQUENCE 168 AA; 18583 MW; 2F2F68317CT103809 CRC64;
SQ
Query Match 27.3%; Score 296; DB 1; Length 168;
Best Local Similarity 44.3%; Pred. No. 9, 5e-17;
Matches 62; Conservative 15; Mismatches 51; Indels 12; Gaps 3;
QY 69 EYLAHPNARAANGVAPLRNMGASAAAGTYAQQRRGGCAFPADVGA----SPYGANG 124
DB 36 DYDAHNTARADVGEPLTWDDQVAAAYAAQNTYSQ-----LAADCNLVHSHGQYENLA 88
QY 125 WASYR-ARPAEVVALMVAEGRYTHANNTCAGRCQCTYTQVWRRNTAEVGCAQASCATG 183

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Db 89 WSSGDFLTAKAVEMVNEKQYVANDSMTCAQGVCHYTQVWVRNSVRGACAVOCNNG 148

QY 184 ATTLCLYNPHGVQGSPEY 203

Db 149 GYIVSCNTPDPGNVIGKSPY 168

# RESULT 5

PR12\_HORVU STANDARD: PRT: 164 AA.

AC P35752;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Pathogenesis-related protein PR1-2 precursor.  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Trilicaceae; Hordeum.  
OX NCBI\_taxid=4513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV, PSAKNON RESISTANT; TISSUE=leaf;  
RX MEDLINE=95036024; PubMed=7524728;  
RA Mouradov A., Mouradova E., Scott K.J.;  
RT "gene family encoding basic pathogenesis-related 1 proteins in  
barley.";  
RL Plant Mol. Biol. 26:503-507(1994).  
CC - FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS  
CC AGAINST PATHOGENS.  
CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;  
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.

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DR EMBL: Z26320; CAA81229.1; -  
DR PIR: S37188; S37188.  
DR HSSP: P04284; 1CFE.  
DR InterPro: IPR001283; Allrgn\_V5/TPx1.  
DR Pfam: PF00188; SCP\_1.  
DR PRINTS: PR00837; V5TPX1KE.  
DR ProDom: PD000542; Allrgn\_V5/TPx1; 1.  
DR SMART: SM00198; SCP\_1.  
DR PROSITE: PS01009; SCP\_AGS\_PRL\_SC7\_1; 1.  
DR PROSITE: PS01010; SCP\_AGS\_PRL\_SC7\_2; 1.  
KW Plant defense; Pathogenesis-related protein; signal; multigene family.  
FT SIGNAL 1 24  
FT CHAIN 25 164  
FT MOD\_RES 25 25  
FT DISULFID 68 140  
FT DISULFID 113 119  
FT DISULFID 135 150  
SQ SEQUENCE 164 AA: 17679 MW; DBF722DB74EE390 CRC64;

Query Match 26.8%; Score 290.5; DB 1; Length 164;  
Best Local Similarity 39.1%; Pred. No. 2.5e-16;  
Matches 72; Conservative 22; Mismatches 61; Indels 29; Gaps 8;

QY 24 LATLLALCAAPATTHGARYLMFGAGAVTKAQQSGTSNATYADELIARHNARAAVY 83

Db 6 LATLLALAMAAAVN-----LSQAN-----SPQDYVSPHNAARSVGV 44

QY 84 APLRWNAAGLASAAGTVAOORGGCAFDVAGSPYGANOGMASTYRA--PRAEYVALMVA 141

Db 45 GAVSWSTKL-QAFAYQNYANG-RINDCKLQHSQ-GPYGENITWGSAGADWKAADAVNSWV 101

QY 142 EGRYTHANNTCAAGRGCGTQVWVRNPAVYCAQASCAT--GATLECLYNPHGVQGS 199

Db 102 EKKDYNIGSMTCAKGVCHYTQVWVRNSTIGCAVYCNRRGVFT-CNYEPKNGV 160

QY 200 QSPY 203

Db 161 QKPY 164

# RESULT 6

PR12\_HORVU STANDARD: PRT: 164 AA.

AC Q05968;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Pathogenesis-related protein 1 precursor.  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Trilicaceae; Hordeum.  
OX NCBI\_taxid=4513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=94033324; PubMed=8219079;  
RA Mouradov A., Petrasovits L., Davidson A., Scott K.J.;  
RT "A cDNA clone for a pathogenesis-related protein 1 from barley.";  
RL Plant Mol. Biol. 23:439-442(1993).  
CC - FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS  
CC AGAINST PATHOGENS.  
CC - SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;  
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.

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DR EMBL: Z21494; CAA9703.1; -  
DR PIR: S32002; S32002.  
DR PIR: S39474; S39474.  
DR HSSP: P04284; 1CFE.  
DR InterPro: IPR001283; Allrgn\_V5/TPx1.  
DR Pfam: PF00188; SCP\_1.  
DR PRINTS: PR00837; V5TPX1KE.  
DR ProDom: PD000542; Allrgn\_V5/TPx1; 1.  
DR SMART: SM00198; SCP\_1.  
DR PROSITE: PS01009; SCP\_AGS\_PRL\_SC7\_1; 1.  
DR PROSITE: PS01010; SCP\_AGS\_PRL\_SC7\_2; 1.  
KW Plant defense; Pathogenesis-related protein; signal; multigene family.  
FT SIGNAL 1 24  
FT CHAIN 25 164  
FT MOD\_RES 25 25  
FT DISULFID 68 140  
FT DISULFID 113 119  
FT DISULFID 135 150  
SQ SEQUENCE 164 AA: 17683 MW; 80972FE654F77395 CRC64;

Query Match 26.6%; Score 288.5; DB 1; Length 164;  
Best Local Similarity 38.6%; Pred. No. 3.6e-16;  
Matches 71; Conservative 24; Mismatches 60; Indels 29; Gaps 8;

QY 24 LATLLALCAAPATTHGARYLMFGAGAVTKAQQSGTSNATYADELIARHNARAAVY 83

Db 6 LATLLALAMAAAVN-----LSQAN-----SPQDYVSPHNAARSVGV 44

QY 84 APLRWNAAGLASAAGTVAOORGGCAFDVAGSPYGANOGMASTYRA--PRAEYVALMVA 141

Db 45 GAVSWSTKL-QAFAYQNYANG-RINDCKLQHSQ-GPYGENITWGSAGADWKAADAVNSWV 101

```

OY 142 EGRYTHANNTCAGRCGCTGYOVWNRANTAEVGAQASCAT--GATLTLCLYNPHGNVG 199
DB 102 EKDYDVGSTNCAKGVCHYTOVWRASISIGCARVCNNRGVFTI-CNTEPRGNTIG 160
OY 200 QSPY 203
DB 161 OKPY 164

RESULT 7
PRL_ARKATH STANDARD; PRT: 161 AA.
AC P33154;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pathogenesis-related protein 1 precursor (PR-1).
GN AtPG14610 OR T6B13.15.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustoids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=cv Landsberg erecta; TISSUE=leaf;
RX MEDLINE=93005717; PubMed=1392369;
RA Uknes S., Mauch-Mani B., Moyer M., Potter S., Williams S.,
RA Duncher S., Chandler D., Slusarenko A., Ward E., Ryals J.,
RT "Acquired resistance in Arabidopsis."
RL Plant Cell 4:645-656(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Beutis M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Renning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Crasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Niernm W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana."
RL Nature 402:761-768(1999).
CC -1- FUNCTION: PARTIALLY RESPONSIBLE FOR ACQUIRED PATHOGEN RESISTANCE.
CC -1- SUBCELLULAR LOCATION: ACCUMULATES IN THE APOPLAST BEFORE
CC SECRETION.
CC -1- INDUCTION: INDUCED BY 2,6-DICHLOROISONICOTINIC ACID (INA) AND
CC SALICYLIC ACID (POSSIBLY AN ENDOGENOUS SIGNAL FOR ACQUIRED
CC RESISTANCE). STRONGLY INDUCED BY PATHOGEN INFECTION.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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CC -----
DR EMBL: M90508; AAA32863.1; -
DR EMBL: AC005398; AAC69381.1; -
DR PIR: J01693; J01693.
DR HSP: P04284; ICFE.
DR InterPro: IPR001283; Allrgn_V5/TPX1.
DR Pfam: PF00188; SCP_1.
DR PRINTS: PR00837; VSTPLIKE.
DR PRODOM: PD000542; Allrgn_V5/TPX1; 1.
DR SMART: SM00198; SCP_1.

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DR PROSITE: PS01009; SCP_AGS_PRL_SC7_1; 1.
DR PROSITE: PS01010; SCP_AGS_PRL_SC7_2; 1.
KW Plant defense; Signal; Pathogenesis-related protein.
FT SIGNAL 1 26
FT CHAIN 27 161
FT MOD_RES 27 27
FT DISULFID 70 138
FT DISULFID 113 117
FT DISULFID 133 147
FT SEQUENCE 161 AA; 17677 MW; 898B0F6347C3F84 CRC64;
SQ
Query Match 26.5%; Score 288; DB 1; Length 161;
Best Local Similarity 39.5%; Pred. No. 3.9e-16;
Matches 64; Conservative 19; Mismatches 65; Indels 14; Gaps 5;

OY 42 YLMPGAGAVYKAOOGGSGSNRTADEYLAIPNORAAVGAFLRMNAGLASAAGIVA 101
DB 14 VALGALVLPKAD-----SPDYLRVHNRAGAVGVGPQWDERVA-AIARSA 63
OY 102 QORRGCAFADVAGSPYGANOGWASYRARPAEVALMVAEGRYVTHANNTCAGRCGT 161
DB 64 EQLR-GNCRLLHSG-GPYGENTLAWGSDLSGSAVMWVSEKANYVYANTC--NGVCGH 119
OY 162 YTOVWNRANTAEVGAQASCATGATLTLCLYNPHGNVQSPY 203
DB 120 YTOVWNRVRLSCAKVCKNNGGTLISCNYPKGVNKEPY 161

RESULT 8
PRLA_TOBAC STANDARD; PRT: 168 AA.
AC P08299;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pathogenesis-related protein 1A precursor (PR-1A).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; easterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_Taxid=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv Samsun NN;
RX MEDLINE=88015528; PubMed=3658669;
RA Cornelissen B.J.C., Horowitz J., van Kan J.A.L., Goldberg R.B.,
RA Bol J.F.;
RT "Structure of tobacco genes encoding pathogenesis-related proteins
RT from the PR-1 group."
RL Nucleic Acids Res. 15:6799-6811(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv Samsun NN;
RX MEDLINE=88083595; PubMed=3691804;
RA Ohsima M., Matsuka M., Yamamoto N., Tanaka Y., Kano-Murakami Y.,
RA Ozei Y., Kato A., Harada N., Ohsashi Y.;
RT "Nucleotide sequence of the PR-1 gene of Nicotiana tabacum."
RL PDB Jett. 225:243-246(1987).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv Wisconsin 38;
RA Pflizer U.M., Pflizer A.J.P., Goodman H.M.;
RT "DNA sequence analysis of a PR-1a gene from tobacco: molecular
RT relationship of heat shock and pathogen responses in plants."
RL Mol. Gen. Genet. 211:290-295(1988).
RN [4]
RP SEQUENCE OF 4-168 FROM N.A.
RC STRAIN=cv Xanthi;
RX MEDLINE=89041576; PubMed=3186451;
RA Cui J.R., Dixon D.D., Carr J.P., Kleesig D.F.;
RT "Isolation and nucleotide sequence of cDNA clones for the
RT pathogenesis-related proteins PRLa, PRLb and PRLc of Nicotiana

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RT tabacum cv. Xanthi nc induced by TMV infection."
RL Nucleic Acids Res. 16:9861-9861(1988).
RN [5]
RP SEQUENCE OF 30-70, 103-131 AND 157-168.
RA Lucas J., Camacho Henriquez A., Lottspeich F., Henschen A.,
RA Sanger H.L.
RT "Amino acid sequence of the 'pathogenesis-related' leaf protein p14
RT from virulent-infected tomato reveals a new type of structurally
RT unfamiliar proteins."
RL EMBO J. 4:2745-2749(1985).
RN [6]
RP SUBCELLULAR LOCATION.
RX MEDLINE-91224081; PubMed=2026137;
RA Dixon D.C., Cutt J.R., Klessig D.F.;
RT "Differential targeting of the tobacco PR-1 pathogenesis-related
RT proteins to the extracellular space and vacuoles of crystal
RT idioblasts."
RL EMBO J. 10:1317-1324(1991).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
CC AGAINST PATHOGENS.
CC -1- SUBCELLULAR LOCATION: ACCUMULATE IN WITHIN THE VACUOLES OF
CC SPECIALIZED CELLS KNOWN AS CRYSTAL IDIOBLASTS.
CC -1- INDUCTION: SYNTHESIZED DURING PATHOGEN INFECTION OR OTHER STRESS-
CC RELATED RESPONSES.
CC -1- PTM: THREE DISULFIDE BONDS ARE PRESENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
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CC -----
DR EMBL; X05959; CAA29392.1; -
DR EMBL; X06361; CAA29660.1; -
DR EMBL; X12485; CAA31008.1; -
DR EMBL; X06930; CAA30017.1; -
DR PIR; S00513; S00513.
DR PIR; A05264; A05264.
DR HSSP; P04284; ICPE.
DR InterPro; IPR001283; Allrgn_V5/TPx1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPX1IKE.
DR ProDom; PD000542; Allrgn_V5/TPx1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; SCP_AG5_PRL_SCP_2; 1.
DR PROSITE; PS01010; SCP_AG5_PRL_SCP_2; 1.
KW Plant defense; Pathogenesis-related protein; Multigene family; Signal.
FT SIGNAL 1 30
FT CHAIN 1 168
FT CONFLICT 5 6 LE -> VS (IN REF. 4).
FT CONFLICT 57 57 D -> S (IN REF. 5).
FT CONFLICT 68 69 SO -> PS (IN REF. 5).
FT CONFLICT 106 106 D -> N (IN REF. 3).
FT CONFLICT 153 153 S -> F (IN REF. 3).
FT CONFLICT 162 162 Y -> W (IN REF. 5).
SQ SEQUENCE 168 AA; 18573 MW; 2737521703129280 CRC64;
Query Match 26.4%; Score 286; DB 1; Length 168;
Best local Similarity 36.7%; Pred. No. 5; Ee -16;
Matches 69; Conservative 22; Mismatches 59; Indels 38; Gaps 7;
OY 22 LILATLALCAPAPTHGKRVLMFGAGAVTKAQQGGTSSNATADERYLAPNQRRAV 81
DB 13 LILVSTLLFLVY---SHSCR-----AQNSQ-----DYDANTNTADY 48
OY 82 GVAPLFWNAGLSAAGATYACQROGCGCAFADVGA---SPYGAN--QGWAASRAPAEV 135
DB 49 GVEPLTWDDQVAAYVQNTASQ-----LAADCNLVSHQGYGNLAEGSGDPMY-AAKA 100

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OY 136 VALMAVGRYTHANNTCAAGRCCTYQVWVRNTAEVCAQASCATATLTLCLYNPG 195
DB 101 VEMWVDEKQYDHDNSTCAQGVCGHYTYVWRNSVRYGARVCNNGYVSCNTDPG 160
OY 196 NVGQGSFY 203
DB 161 NYRGESPY 168
RESULT 9
PRL3_HORVU
ID PRL3_HORVU STANDARD; PRT; 164 AA.
AC P35793;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pathogenesis-related protein PRL3-3 precursor (PR-1b) (HV-8).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Pskakon resistant, and cv. NK1558; TISSUE=Leaf;
RX MEDLINE-95036024; PubMed=7524728;
RA Mouradov A., Mouradova F., Scott K.J.;
RT "Gene family encoding basic pathogenesis-related 1 proteins in
RT barley."
RL Plant Mol. Biol. 26:503-507(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Pallas; TISSUE=Leaf;
RX MEDLINE-94281675; PubMed=8012045;
RA Byrgeleson T., Sommer Knudsen J., Gregersen P.L., Collinge D.B.,
RA Ek B., Thordar-Christensen H.;
RT "Purification, characterization, and molecular cloning of basic PR-1-
RT type pathogenesis-related proteins from barley."
RL Mol. Plant Microbe Interact. 7:267-275(1994).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
CC AGAINST PATHOGENS.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
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CC -----
DR EMBL; Z26321; CAA81230.1; -
DR EMBL; Z26333; CAA81234.1; -
DR EMBL; X74940; CAA52894.1; -
DR PIR; S37189; S37189.
DR PIR; S37209; S37209.
DR PIR; S37167; S37167.
DR HSSP; P04284; ICPE.
DR InterPro; IPR001283; Allrgn_V5/TPx1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPX1IKE.
DR ProDom; PD000542; Allrgn_V5/TPx1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; SCP_AG5_PRL_SCP_2; 1.
DR PROSITE; PS01010; SCP_AG5_PRL_SCP_2; 1.
KW Plant defense; Pathogenesis-related protein; Signal; Multigene family.
FT SIGNAL 1 24
FT CHAIN 1 164
FT MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID
FT DISULFID 68 140
FT 113 119 BY SIMILARITY.

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RP STRUCTURE BY NMR.
RX MEDLINE=97220236; PubMed=9067611;
RA Fernandez C., Szyperiski T., Bruyere T., Ramage P., Moesinger E.,
RA Wuehlisch K.;
RT "NMR solution structure of the pathogenesis-related protein p14a.";
RL J. Mol. Biol. 266:576-593(1997).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
CC AGAINST PATHOGENS. HAS ANTIFUNGAL ACTIVITY.
CC -1- DEVELOPMENTAL STAGE: MAXIMUM EXPRESSION FOUND DURING DAYS 4 TO 8
CC AND DAYS 8 TO 12 AFTER INOCULATION WITH AN AVIRULENT AND A
CC VIRULENT PATHOGEN RESPECTIVELY.
CC -1- INDUCTION: UPON INFECTION BY VIRULENT AND AVIRULENT RACES OF
CC PATHOGENS, FOR EXAMPLE FUNGAL PATHOGEN C. FRUITVOM. ALSO INDUCED BY
CC ETHYLENE.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SCF/SC14 AND PLANTS PR-1.
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CC -----
DR EMBL: M69248; AAA03616.1; -
DR EMBL: X68738; CAA8672.1; -
DR EMBL: Y08804; CAA70042.1; -
DR PIR: A03379; VCT014.
DR PIR: S26379; S26239.
DR PIR: S29628; S29628.
DR PDB: 1CFE; 12-NOV-97.
DR InterPro: IPR001283; Allrgn_V5/TPx1.
DR Pfam: PF00188; SCP: 1.
DR PRINTS: PRO00837; V5TPXLIKE.
DR PRODOM: PD000542; Allrgn_V5/TPx1; 1.
DR SMART: SM00198; SCP: 1.
DR PROSITE: PS01009; SCP_AG5_PRL_SCF_1; 1.
DR PROSITE: PS01010; SCP_AG5_PRL_SCF_2; 1.
KW Plant defense; Pathogenesis-related protein; signal; Multigene family;
KW Fungicide; 3D-structure.
FT SIGNAL 1 24
FT CHAIN 25 159 PATHOGENESIS-RELATED LEAF PROTEIN 6.
FT MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 68 136
FT DISULFID 109 115
FT DISULFID 131 145
FT CONFLICT 123 127 MISSING (IN REF. 4).
SQ SEQUENCE 159 AA; 17520 MW; EA55AC3AC0FEF3F4 CRC64;

Query Match 25.6% Score 277.5; DB: 1; Length 159;
Best Local Similarity 44.5%; Pred. No. 2.6e-15;
Matches 61; Conservative 13; Mismatches 54; Indels 9; Gaps 4;

QY 69 EYLA PHNQARA VAVAPLEFMNGLASAAAGTVAQQRGGSCAFADVGASPYGAN--QGMVA 126
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 30 DYLA VHHNDARAQVGVPMGMDANLASRAQNYA--NSRAGDCNLTLSGA--GENLAKGGG 84
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 127 SYRARPPEVVALWVAGRGYYTHANNNTCAAGRCGGYTVGVVRRNRAEYGAQAQASCAAGATL 186
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 85 DFTGRAA--VQLVWSERPSTYNTATNQCVGKKCRHITYVVRNRSYRLGCGRACNNGWVF 142
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 187 TLCLYNPHGNVQGSPPY 203
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 143 ISCNVDYDVGWNIQGRPY 159
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
PRL_MEDTR
ID PRL_MEDTR STANDARD; PRT: 173 AA.
AC Q40374;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

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DT 15-JUN-2002 (Rel. 4), last annotation update)
DE Pathogenesis-related protein PR-1 precursor.
GN PR-1.
OS Medicago truncatula (barrel medic).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
OX NCBI_TaxID=3880;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Root.
RA MEDLINE=95175606; PubMed=7870819;
RA Szylak-Strozycka U., Lescur N., Cullimore J.V., Gamas P.;
RA "A cDNA encoding a PR-1-like protein in the model legume Medicago
RT truncatula."
RL Plant Physiol. 107:273-274(1995).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
CC AGAINST PATHOGENS.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
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CC -----
DR EMBL; X79778; CAA56174.1; -
DR HSSP; P04284; ICFE.
DR Interpro; IPR001283; Allrgn_V5/7pxl.
DR Pfam; PF00188; SCP. 1
DR PRINTS; PR00837; V5TPXLIKE.
DR PRODOM; PD000542; Allrgn_V5/7pxl; 1.
DR SMART; SM00198; SCP. 1.
DR PROSITE; PS01009; SCP_AGS_PRI_SCP_1; 1.
DR PROSITE; PS01010; SCP_AGS_PRI_SCP_2; 1.
KW Plant defense; Pathogenesis-related protein; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 1 23 PATHOGENESIS-RELATED PROTEIN PR-1.
FT DISULFID 78 149 BY SIMILARITY.
FT DISULFID 122 128 BY SIMILARITY.
FT DISULFID 144 159 BY SIMILARITY.
SQ SEQUENCE 173 AA; 19760 MW; 898B00C9CD72DE4A CRC64;

Query Match 24.7%; Score 268.5; DB 1; Length 173;
Best Local Similarity 42.0%; Pred. No. 1.4e-14;
Matches 60; Conservative 19; Mismatches 59; Indels 5; Gaps 5;

OY 63 SNATADBYLAPHNOARAAGVAPLRNNAAGTAAQRRGGCAEFADVASPYGAN 122
DB 34 SRSEFNOLLPONTARAAGVLRPLVMDKLTHTAQ-WYANORR-MDCAL-EHSNPNYGEN 90
OY 123 OGMA5-YRAREAEVVALVMEGRYTHANNTCAGRCGCTYQVWRNTAEVGCAGQASC 181
DB 91 IFMGSGVMNNAQAVASAVDEKOFYNTWNSVCVDGEMCHTYQVWGSTTKGCA5VCS 150
OY 182 TG-ATLTLCLYNPHGNVQGSPPY 203
DB 151 DDGTFMTCNYDPGPNYNGERP 173

RESULT 14
PR1L_TOBAC STANDARD; PRT; 177 AA.
AC P11670.
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DE Basic form of pathogenesis-related protein 1 precursor (PR 1).
OS Nicotiana tabacum (Common tobacco).
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Xanthi;
RA Payne G., Middlesteadt W., Desai N., Williams S., Dincher S.,
RA Carnes M., Ryals J.;
RA "Isolation and sequence of a genomic clone encoding the basic form of
RT pathogenesis related protein 1 from Nicotiana tabacum."
RL Plant Mol. Biol. 12:595-596(1989).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
CC AGAINST PATHOGENS.
CC -1- PTM: TWO DISULFIDE BONDS ARE PRESENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
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CC -----
DR EMBL; X14065; CAA32228.1; -
DR PIR; S04728; S04728.
DR HSSP; P04284; ICFE.
DR Interpro; IPR001283; Allrgn_V5/7pxl.
DR Pfam; PF00188; SCP. 1.
DR PRINTS; PR00837; V5TPXLIKE.
DR PRODOM; PD000542; Allrgn_V5/7pxl; 1.
DR SMART; SM00198; SCP. 1.
DR PROSITE; PS01009; SCP_AGS_PRI_SCP_1; 1.
DR PROSITE; PS01010; SCP_AGS_PRI_SCP_2; 1.
KW Plant defense; Pathogenesis-related protein; Multigene family; Signal.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 177 BASIC FORM OF PATHOGENESIS-RELATED
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID
FT FT (BY SIMILARITY).
SQ SEQUENCE 177 AA; 19729 MW; 3DA58AFB4C206E9 CRC64;

Query Match 24.0%; Score 260; DB 1; Length 177;
Best Local Similarity 39.9%; Pred. No. 6.7e-14;
Matches 57; Conservative 17; Mismatches 65; Indels 4; Gaps 3;

OY 61 SSNATADBYLAPHNOARAAGVAPLRNNAAGTAAQRRGGCAEFADVASPYG 120
DB 21 SKAQNSPDQDYLNPNAARQVGVPMTDNRNLAAYQNVANQ-RIGDGMTH-SHGPG 77
OY 121 ANOGASVYRAREAEVVALVMEGRYTHANNTCAGRCGCTYQVWRNTAEVGCAGASC 180
DB 78 ENLAAPQOLNAGAAGVKKMWDERFRDYNSNCVGG-VGCHTYQVWRNSVRLGCAVRAS 136
OY 181 ATGATLTLCLYNPHGNVQGSPPY 203
DB 137 NNGWEFTTCNYDPGPNYNGERP 159

RESULT 15
PR1A_LYCES STANDARD; PRT; 175 AA.
AC O08697.
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Pathogenesis-related protein 1A1 precursor (PR-1A1).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;

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OM protein - protein search, using sw model

Run on: March 19, 2003, 09:35:38 ; Search time 30 Seconds  
(without alignments)  
1394.252 Million cell updates/sec

Title: US-09-832-320-2  
Perfect score: 1085  
Sequence: 1 MAHSRSHHLLLPAPMATA.....ATLTCLYNPHGNVGQSPY 203

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SPREMBL\_21:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID     | Description        |
|------------|-------|-------------|--------|--------|--------------------|
| 1          | 348.5 | 32.1        | 185    | 09FYU1 | 09FYU1 arabidopsis |
| 2          | 331   | 30.5        | 163    | 082086 | 082086 zea mays (m |
| 3          | 325.5 | 30.0        | 191    | 092XN5 | 092XN5 camellia si |
| 4          | 313.5 | 28.9        | 164    | 09XH05 | 09XH05 arabidopsis |
| 5          | 309   | 28.5        | 167    | 08W084 | 08W084 oryza sativ |
| 6          | 308.5 | 28.4        | 164    | 043489 | 043489 hordeum vul |
| 7          | 307.5 | 28.3        | 172    | 10     | 081889 arabidopsis |
| 8          | 304   | 28.0        | 164    | 040597 | 040597 nicotiana t |
| 9          | 303.5 | 28.0        | 169    | 10     | 039188 arabidopsis |
| 10         | 302.5 | 27.9        | 179    | 10     | 004106 arabidopsis |
| 11         | 297.5 | 27.4        | 163    | 10     | 081888 arabidopsis |
| 12         | 296.5 | 27.3        | 164    | 10     | 082714 triticum ae |
| 13         | 294   | 27.1        | 166    | 10     | 039187 arabidopsis |
| 14         | 293.5 | 27.1        | 164    | 10     | 094F73 arabidopsis |
| 15         | 291.5 | 26.9        | 140    | 10     | 08S3W2 cucumis sat |
| 16         | 288.5 | 26.6        | 159    | 10     | 0941G6 solanum tub |

|    |       |      |     |    |                    |
|----|-------|------|-----|----|--------------------|
| 17 | 288   | 26.5 | 162 | 10 | 096344 brassica na |
| 18 | 288   | 26.5 | 183 | 10 | 09LNU2 arabidopsis |
| 19 | 287.5 | 26.5 | 159 | 10 | 09SC15 solanum tub |
| 20 | 285   | 26.3 | 205 | 10 | 09L212 arabidopsis |
| 21 | 284   | 26.2 | 168 | 10 | 09FE57 oryza sativ |
| 22 | 284   | 26.2 | 179 | 10 | 09AT44 capsicum an |
| 23 | 283   | 26.1 | 168 | 10 | 040557 nicotiana t |
| 24 | 281   | 25.9 | 168 | 10 | 040397 nicotiana g |
| 25 | 275.5 | 25.4 | 185 | 10 | 08W3X9 solanum tor |
| 26 | 271   | 25.0 | 185 | 10 | 09SV22 arabidopsis |
| 27 | 269.5 | 24.8 | 207 | 10 | 09FKL1 arabidopsis |
| 28 | 269   | 24.8 | 190 | 10 | 09SW05 arabidopsis |
| 29 | 265.5 | 24.5 | 161 | 10 | 09ZNS4 arabidopsis |
| 30 | 264.5 | 24.4 | 173 | 10 | 082715 triticum ae |
| 31 | 263.5 | 24.3 | 161 | 10 | 043392 brassica na |
| 32 | 261.5 | 24.1 | 174 | 10 | 040035 hordeum vul |
| 33 | 260.5 | 24.0 | 164 | 10 | 004000 oryza sativ |
| 34 | 260.5 | 24.0 | 186 | 10 | 09SF44 arabidopsis |
| 35 | 259.5 | 23.9 | 160 | 10 | 024026 lycopersico |
| 36 | 257   | 23.7 | 161 | 10 | 09MOC8 arabidopsis |
| 37 | 256.5 | 23.6 | 210 | 10 | 09SW04 arabidopsis |
| 38 | 253.5 | 23.4 | 142 | 10 | 09LJ44 pyrus pyrif |
| 39 | 249.5 | 23.0 | 161 | 10 | 09LJMS arabidopsis |
| 40 | 246   | 22.7 | 176 | 10 | 039186 arabidopsis |
| 41 | 243   | 22.4 | 161 | 10 | 09LPM7 arabidopsis |
| 42 | 242.5 | 22.4 | 120 | 10 | 09LJ55 pyrus pyrif |
| 43 | 242   | 22.3 | 168 | 10 | 024025 lycopersico |
| 44 | 242   | 22.3 | 177 | 10 | 065157 capsicum an |
| 45 | 234   | 21.6 | 162 | 10 | 09LPM6 arabidopsis |

#### ALIGNMENTS

RESULT 1  
Q9FYU1 PRELIMINARY; PRT; 185 AA.  
ID Q9FYU1  
AC Q9FYU1:  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Similarity to pathogenesis-related protein (unknown protein)  
DE (Hypothetical 20.1 kDa protein).  
GN KLF13.27 OR AFS66590.  
GN Arabidopsis thaliana (Mouse-ear cress).  
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=COLUMBIA;  
RX MEDLINE=98403884; PubMed=9734815;  
RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,  
RA Tabata S.;  
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.  
RT Physically assigned PI and TAC clones.";  
RT DNA Res. 5:203-216(1998).  
RL [2]  
RN SEQUENCE FROM N.A.  
RA Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,  
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,  
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,  
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,  
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,  
RA Ecker J., Theologis A., Davis R.W.;  
RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,  
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,  
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,



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09XH05
ID Q9XH05 PRELIMINARY; PRT; 164 AA.
AC Q9XH05;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
GN TIN24.14 protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Washu;
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Murray J., Langston Y., Clarke K., Drone K.;
RT "The sequence of A. thaliana TIN24."
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Waterston R.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF149413; AAD40121.1; -.
DR HSSP: P04284; ICFF.
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP; 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR ProDom: PD000542; Allrgn_V5/Tpx1; 1.
DR SMART: SM00198; SCP; 1.
DR PROSITE: PS01009; SCP_AG5_PRL_SC7_1; 1.
DR PROSITE: PS01010; SCP_AG5_PRL_SC7_2; 1.
SQ SEQUENCE 164 AA; 18397 MW; 840F99DB9FA7DF39 CRC64;

Query Match 28.9%; Score 313.5; DB 10; Length 164;
Best Local Similarity 46.3%; Pred. No. 2.5e-16;
Matches 63; Conservative 18; Mismatches 52; Indels 3; Gaps 3;

QY 69 EXLAPHNQAARAAGVAPLPMNAGLASAAAGTAAQOROGGCAAFADYVQSP-YGANQGNAS 127
DB 31 DYLDENNRARTQGVPPMKWNG-AEQYAMNAAQQRK-GDCSLTSHNSNGLYGENTLANS 88
QY 128 YKARPAEYVALVVAEGRIYTHANNNTCAAGROCGTYTVVWRNTAEVGCQAQSCATGATLT 187
DB 89 GALSQAELAVKLMVYNEKSDIYASNTCSDGKCGHYTVVWRTSEWVGCAKVKCDNGTFFV 148
QY 188 LCLYNPHGNVQSGSPY 203
DB 149 TCNYPPPGNYKGRWMPY 164

RESULT 5
Q8W084 PRELIMINARY; PRT; 167 AA.
AC Q8W084;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Putative pathogenesis-related protein.
GN OSJNBA0091E23.7.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Saeki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
RT clone:OSJNBA0091E23."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP003853; BAB84473.1; -.
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP; 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR ProDom: PD000542; Allrgn_V5/Tpx1; 1.
DR SMART: SM00198; SCP; 1.
DR PROSITE: PS01009; SCP_AG5_PRL_SC7_1; UNKNOWN.1.
DR PROSITE: PS01010; SCP_AG5_PRL_SC7_2; UNKNOWN.1.
SQ SEQUENCE 167 AA; 18334 MW; 40AE3EA7284433D2E CRC64;

Query Match 28.5%; Score 309; DB 10; Length 167;
Best Local Similarity 40.1%; Pred. No. 5.5e-16;
Matches 73; Conservative 21; Mismatches 68; Indels 20; Gaps 7;

QY 25 ATLLALCAAPPTTGARYLMFGAGAYTKAQQGTSGSNATADEYLAAPHNQAARAAGVA 84
DB 3 ASKLALICS-----LFLV-----AVYAATMFHCSDAQNPSQD-YLSPQNAARSAGVYG 48
QY 85 PLRWNAGLASAAGTAAQOROGGCAAFADYVQSPYGANQGNASVRA--RAEYVALVVAE 142
DB 49 PMSMSTKIQGFADYARQ--RKGDCLQHSG-GPYGENIFGSGADWTAADAVRSWDE 105
QY 143 GRYTTHANNNTCAAGROCGTYTVVWRNTAEVGCQAQASC-ATGATLTCLYNPHGNVQSGOS 201
DB 106 KKYNYASNSCAAGKVCGHYTVVWRDSTNVCAGRVACDNRGFIICNENPGRNIVGR 165
QY 202 PY 203
DB 166 PY 167

RESULT 6
Q43489 PRELIMINARY; PRT; 164 AA.
AC Q43489;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE PR-1a pathogenesis related protein (Hv-1a) precursor.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. PALLAS; TISSUE=LEAF;
RX MEDLINE=94281675; PubMed=8012045;
RA Bryngelsson T., Sommer-Knudsen J., Gregersen P.L., Collinge D.B.,
RA Ek B., Thordal-Christensen H.;
RT "Purification, characterization and molecular cloning of basic PR-1-
RT type pathogenesis related proteins from barley."
RL Mol. Plant Microbe Interact. 7:267-275(1994).
DR EMBL: X74939; CA452893.1; -.
DR HSSP: P04284; ICFF.
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP; 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR ProDom: PD000542; Allrgn_V5/Tpx1; 1.
DR SMART: SM00198; SCP; 1.
DR PROSITE: PS01009; SCP_AG5_PRL_SC7_1; 1.
DR PROSITE: PS01010; SCP_AG5_PRL_SC7_2; 1.
KW Signal.
FT CHAIN 1 24 POTENTIAL.
FT CHAIN 25 164 PR-1A PATHOGENESIS RELATED PROTEIN
SQ SEQUENCE 164 AA; 17440 MW; 063F219DEFEB7E548 CRC64;

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[illegible]

PR 06-MAY-1999; 99US-0132487.  
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PR 14-MAY-1999; 99US-0134218.  
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PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
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PR 24-MAY-1999; 99US-0135629.  
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PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
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PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
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PR 16-JUL-1999; 99US-0144085.  
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PR 27-AUG-1999; 99US-0151065.  
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PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
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PR 22-SEP-1999; 99US-0155139.  
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PR 24-SEP-1999; 99US-0155659.  
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PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
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PR 21-OCT-1999; 99US-0160767.  
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PR 21-OCT-1999; 99US-0160814.

CC This sequence represents the maize PR-1 like protein, PR-1mz. The cDNA  
CC encoding this sequence was isolated by screening a BTH-induced cDNA  
CC library of maize. The library was screened using a probe matching to  
CC the PR-1 barley clone HVPRI8R. The cDNA encoding this sequence,

PT New promoter sequences from pathogenesis-related genes of maize -  
XX  
PS Example 3; Page 73-74; 86pp; English.  
XX  
AA221186 to AA221190 represents the nucleotide sequences for promoters





PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
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PR 03-JUN-1999; 99US-0137528.  
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PR 16-JUL-1999; 99US-0144086.  
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PR 23-AUG-1999; 99US-0149930.  
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PR 22-OCT-1999; 99US-0160981.  
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PR 25-OCT-1999; 99US-0161405.  
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PR 26-OCT-1999; 99US-0161360.  
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PR 28-OCT-1999; 99US-0161920.



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PR 02-AUG-1999; 99US-0146388.
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PR 22-OCT-1999; 99US-0160989.
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PR 26-OCT-1999; 99US-0161361.

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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match          29.0%; Score 314.5; DB 21; Length 127;
Best Local Similarity 48.4%; Pred. No. 1.4e-21;
Matches 61; Conservative 15; Mismatches 47; Indels 3; Gaps 2;

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QY 81 VGVADLRNNAGLASAAAGTYAQQROGGCAFADVGASPYGANQGNAS--YRRAPEVAL 138
DB 2 VGVPELVMSQTLFAASRLARQRMKCEFAISLNGKYGANQWAKGVAVTPESLAVET 61
QY 139 WVAEGRYTYTHANNPCAGROCGTYTOVWVWNTAEVGAQASCATGAT-LTLCLYPNHGNV 197
DB 62 WKKEKPEFYNYKSDPCANHTCGYKQVYVWVWNSRELGCATCTKRISYVLTICFNPENI 121
QY 198 QGQSPY 203
DB 122 IGQKPY 127

```

## RESULT 9

```

ID ABB77765 standard; Protein; 161 AA.
XX
AC ABB77765;
XX
DT 20-AUG-2002 (first entry)
XX
DE Amino acid sequence of an antibacterial protein.
XX
KW Antibacterial protein; antibacterial agent; food; plant.
XX
OS Wasabia japonica.
XX
PN JP2002095475-A.
XX
PD 02-APR-2002.
XX
PF 19-SEP-2000; 2000JP-0284178.
XX
PR 19-SEP-2000; 2000JP-0284178.
XX
PA (IWAT-) IWATE KEN.
XX
DR WPI; 2002-439986/47.
XX
DR N-PSDB; ABL59001.
XX
PT New antibacterial protein gene of Wasabia japonica
XX
PS Claim 1; Page 13-14; 17pp; Japanese.
XX
CC The present sequence represents an antibacterial protein of Wasabia
CC japonica. The protein can be used in an antibacterial agent and a
CC functional food.
XX
SQ Sequence 161 AA;

```

```

Query Match          28.0%; Score 304; DB 23; Length 161;
Best Local Similarity 39.8%; Pred. No. 1.8e-20;
Matches 72; Conservative 20; Mismatches 61; Indels 28; Gaps 7;

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```

QY 23 LIALTLALCAAPAPTHGARVLPFGAGAVTKAQQGTGSGSNATDEYLAIPHNOARAIVG 82
DB 9 LILLIALALVGA-----IVLP-----SKAD-----SPQDYLRVHNGRAAVG 45
QY 83 VAPLRNNAGLASAAAGTYAQQROGGCAFADVGASPYGANQGNASTRARPAEVALWAE 142
DB 46 VQPMQWDDRYA-AFARSYADQR-GDCRLTHSG-GPYGNLWMSGSDLSGISAVNMWNE 102
QY 143 GRYTYTHANNPCAGROCGTYTOVWVWNTAEVGAQASCATGATLTLCLYPNHGNVQOGSP 202

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Db 103 KANYTPSNTC--NGVCHTTQVWRNSVRLGCAKVCNNNGTIIYCNIDPFGNYNQRP 160  
 QY 203 Y 203  
 Db 161 Y 161

## RESULT 10

AAFP1059  
 ID AAFP1059 standard; protein; 168 AA.

XX AAFP1059;

DT 21-JUN-1990 (first entry)

DE Nicotiana tabacum pathogenesis-related (P-R) protein encoded by cDNA.

KW Pathogenesis-related protein; Nicotiana tabacum cv. Samsun NN;

KM PNTSNNCPRLC/83.

OS Nicotiana tabacum cv. Samsun NN.

XX Key Location/Qualifiers

FT Peptide 1..30 /note="Signal peptide"

FT Protein 31..168

PN EP307841-A.

PD 22-MAR-1989.

PF 12-SEP-1988; 88EP-0114877.

PR 15-SEP-1987; 87US-0096579.

PA (GEHO-) GEN HOSPITAL CORP.

PI Piltzner UM, Piltzner AP, Goodman HM;

DR WPI; 1989-087235/12.

PT Pathogenesis-related proteins and regulatory sequences -  
 used for expression in plants to enhance hypersensitive response  
 to invading pathogen

PS Fig 4; 32pp; English.

CC It is deduced from cDNA from tobacco mosaic virus (TMV) infected  
 CC tobacco plants contained in plasmid pNCSNNCPRLC/83. Expression of  
 CC a recombinant DNA molecule that encodes P-R proteins and  
 CC regulatory sequences in a plant enhances the hypersensitive response of  
 CC the plant to an invading pathogen. The calculated molecular weight of  
 CC the mature P-R protein is 15,129 and is in reasonable agreement with the  
 CC M<sub>r</sub> of 18kD estimated by SDS polyacrylamide gel electrophoresis.

SO Sequence 168 AA:

Query Match 28.0%; Score 304; DB 10; Length 168;

Best Local Similarity 45.0%; Pred. No. 1.9e-20; Mismatches 50; Indels 12; Gaps 3;

QY 69 EYLAPHNORAAAVGAPLRLMNGLASAAAGTVAQORRGCGCAFADVGA---SPYGANOG 124

Db 36 DYIDAHNTARADYGEPLTWDMGVAAYQNTYASQ-----LAADCNLVHSHGQYGENLA 88

QY 125 WASYR-ARPAEVVALWVAEGRYTHANNTCAGRGCGTYYQVWRNTAEVGAQASCATG 183

Db 89 WSGSDEFTAAKAVEMWVNEKQYTHDSNTCAQGVCGHTTQVWRNSVRYGCARVCCNN 148

QY 184 AFLTLCLYNPHGNVQGSPPY 203

Db 149 GYVSCNIDPFGNYTGSPPY 168

## RESULT 11

AA07314  
 ID AA07314 standard; protein; 138 AA.

XX AA07314;

DT 31-JAN-1991 (first entry)

DE PR-1b plant pathogenesis-related protein.

KW Transgenic plants; disease resistance; chimeric DNA;

XX plant pathogenesis-related protein.

OS synthetic.

PN EP392225-A.

PD 17-OCT-1990.

PF 21-MAR-1990; 90EP-0105336.

PR 20-OCT-1989; 89US-0425504.

PR 24-MAR-1989; 89US-0329018.

PR 20-JUN-1989; 89US-0368672.

PA (CIBA) CIBA GEIGY AG.

PI Ryals JA, Alexander DC, Goodman RM, Melius F, Payne GB;

PI Stinson JR, Neuhaus J-M, Moyer MB;

DR WPI; 1990-313983/42.

DR N-PSDB; AA006181.

PT Inducible pathogenesis-related protein from infected plants.

PS Example 15; page 22; 77pp; English.

CC This is the sequence of the plant pathogenesis-related protein  
 CC (PRP), PR-1b. It confers systemic acquired resistance to plants.  
 CC The corresp. DNA is used, in a chimeric construct, to produce  
 CC transgenic plant cells or -tissues with the ability to regenerate  
 CC into plants which are disease resistant.

CC See also AA006179-80, AA006182-86, AA006199-006208 and AA006829.

SO Sequence 138 AA:

Query Match 27.9%; Score 303; DB 11; Length 138;

Best Local Similarity 46.1%; Pred. No. 1.8e-20; Mismatches 47; Indels 14; Gaps 4;

QY 69 EYLAPHNORAAAVGAPLRLMNGLASAAAGTVAQORRGCGCAFADVGA---SPYGAN-- 122

Db 6 DYIDAHNTARADYGEPLTWDMGVAAYQNTYASQ-----LAADCNLVHSHGQYGENLA 58

QY 123 OGNASYRARPAAEVVALWVAEGRYTHANNTCAGRGCGTYYQVWRNTAEVGAQASCAT 182

Db 59 QGSDEFTAAKAVEMWVNEKQYTHDSNTCAQGVCGHTTQVWRNSVRYGCARVCCNN 117

QY 183 GATLTLCLYNPHGNVQGSPPY 203

Db 118 GGYVSCNIDPFGNYTGSPPY 138

## RESULT 12

AA44003  
 ID AA44003 standard; protein; 139 AA.

XX AA44003;

DT 21-DEC-1999 (first entry)

XX

DE Tobacco pathogenesis related protein #4.  
 XX  
 XX Prediction; secondary structure; alignment; evolutionary conservation;  
 KM homology; periodicity; co-variation analysis; antigenic site;  
 KW site directed mutagenesis; interaction.  
 XX  
 OS Nicotiana tabacum.  
 XX  
 XX US5958784-A.  
 XX  
 XX 28-SEP-1999.  
 XX  
 XX 25-MAR-1992; 92US-0857224.  
 XX  
 XX 25-MAR-1992; 92US-0857224.  
 XX  
 XX 25-MAR-1992; 92US-0857224.  
 XX  
 XX (BENN/) BENNER S A.  
 XX  
 XX Benner SA;  
 XX  
 XX WPI: 1999-570766/48.  
 XX  
 XX Predicting the folded structure of proteins -  
 XX  
 XX Disclosure; Column 371-374; 113pp; English.  
 XX  
 XX Sequences AA43902-Y44015 represent proteins used in a novel method of  
 CC predicting the folded structure of proteins, by aligning sequences of  
 CC homologous proteins and using patterns of evolutionarily conserved and  
 CC varied sequences to assign positions. Positions in the alignment are  
 CC assigned to the surface or inside of the folded structure, active sites,  
 CC and parsing segments. Secondary structural units are assigned by  
 CC identifying periodicity in the assignments, and assembled into globular  
 CC form using distance constraints imposed by disulfide bridges, active  
 CC site assignments and co-variation analysis. The predicted secondary  
 CC structures are useful for identifying antigenic sites on a protein  
 CC molecule, as guides for site directed mutagenesis studies, and for  
 CC understanding the interaction of a protein with other molecules.  
 XX  
 XX Sequence 139 AA;  
 SQ  
 Query Match 27.9%; Score 303; DB 20; Length 139;  
 Best Local Similarity 46.1%; Pred. No. 1.8e-20;  
 Matches 65; Conservative 15; Mismatches 47; Indels 14; Gaps 4;  
 OY 69 EYLAPHNOARRAAYGAPLRNAGLASAAGTVAQORRGCAADYGA-----SPYGAN-- 122  
 Db 7 DVLDAHNRARADYGEPLTMDNGYAAAYAKNTVSG-----LAADCNLVHSHGQYGENLA 59  
 OY 123 OGMASRYRARPFAEYVALMVAEGRYTHANNNTCAAGRCGCTYTYVWMTAEVGCQAQASCAT 182  
 Db 60 QSGSGFMT-AAKAVEMWVDEKQYDHDNSTCAOGYCGHYTYVWMTAEVGCQAQASCAT 118  
 OY 183 GATLTLCLYNPHGNVQOSPY 203  
 Db 119 GGYVWSCNTDPPGNVIGOSPI 139

RESULT 13  
 AA44005  
 ID AA44005 standard; Protein: 141 AA.  
 XX  
 AC AA44005;  
 XX  
 XX 21-DEC-1999 (first entry)  
 XX  
 XX Maize pathogenesis related protein #3.  
 DE  
 XX Prediction; secondary structure; alignment; evolutionary conservation;  
 KM homology; periodicity; co-variation analysis; antigenic site;  
 KW site directed mutagenesis; interaction.  
 XX  
 OS Zea mays.

XX  
 XX US5958784-A.  
 XX  
 XX 28-SEP-1999.  
 XX  
 XX 25-MAR-1992; 92US-0857224.  
 XX  
 XX 25-MAR-1992; 92US-0857224.  
 XX  
 XX 25-MAR-1992; 92US-0857224.  
 XX  
 XX (BENN/) BENNER S A.  
 XX  
 XX Benner SA;  
 XX  
 XX WPI: 1999-570766/48.  
 XX  
 XX Predicting the folded structure of proteins -  
 XX  
 XX Disclosure; Column 375-376; 113pp; English.  
 XX  
 XX Sequences AA43902-Y44015 represent proteins used in a novel method of  
 CC predicting the folded structure of proteins, by aligning sequences of  
 CC homologous proteins and using patterns of evolutionarily conserved and  
 CC varied sequences to assign positions. Positions in the alignment are  
 CC assigned to the surface or inside of the folded structure, active sites,  
 CC and parsing segments. Secondary structural units are assigned by  
 CC identifying periodicity in the assignments, and assembled into globular  
 CC form using distance constraints imposed by disulfide bridges, active  
 CC site assignments and co-variation analysis. The predicted secondary  
 CC structures are useful for identifying antigenic sites on a protein  
 CC molecule, as guides for site directed mutagenesis studies, and for  
 CC understanding the interaction of a protein with other molecules.  
 XX  
 XX Sequence 141 AA;  
 SQ  
 Query Match 27.6%; Score 299; DB 20; Length 141;  
 Best Local Similarity 42.4%; Pred. No. 4.4e-20;  
 Matches 61; Conservative 16; Mismatches 61; Indels 6; Gaps 4;  
 OY 63 SNTADEYIAPINORAAVGYAPLRNAGLASAAGTVAQORRGCAADYGAASPYCAN 122  
 Db 1 SENSPODYLTTPONSARAAYGVGPVTWSTKLQGFEEKYAAQ--RAGDCRLQHSQ-GPYGN 57  
 OY 123 OGM--ASYRARPFAEYVALMVAEGRYTHANNNTCAAGRCGCTYTYVWMTAEVGCQAQASC 180  
 Db 58 IWMGSAGFDMKAVDAVRSMWDEKQMYNATNCSAAGVCGHYTYVWMTAEVGCQAQASC 117  
 OY 181 ATG-ATLTLCLYNPHGNVQOSPY 203  
 Db 118 RDNRGVFIIICNTEPRGNTAGMKPY 141

RESULT 14  
 AA42365  
 ID AA42365 standard; Protein: 163 AA.  
 XX  
 AC AA42365;  
 XX  
 XX 18-OCT-2000 (first entry)  
 XX  
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 52828.  
 DE  
 XX Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 XX EP1033405-A2.  
 XX  
 XX 06-SEP-2000.  
 XX  
 XX 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 23-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
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PR 04-MAY-1999; 99US-0132484.  
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PR 06-MAY-1999; 99US-0132486.  
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PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
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PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0135124.  
PR 20-MAY-1999; 99US-0135124.  
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PR 24-MAY-1999; 99US-0135629.  
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PR 21-JUN-1999; 99US-0139817.  
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PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
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PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
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PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.

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PR 21-JUL-1999; 99US-0145086.  
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PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
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PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.

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PR 04-OCT-1999; 99US-0157117.
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PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
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PR 14-OCT-1999; 99US-0159330.
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PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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QY 129 RARPAEVVALVVAEGRIYTHANNNTCAAGROCGTYYQVWRNTAEVGAQAQASCATGATLTL 188
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DB 89 SMTGVAADVMDVDEQFDYDSDNTCAWDKCGHYTQVWRNSERLGCACAKRCNNGOTFIT 148

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DB 149 CNYDEPGNMVGEMPY 163

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ID AAR08224 standard; protein: 138 AA.
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DE PR-1c plant pathogenesis-related protein.
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KW Transgenic plants; disease resistance; chimeric DNA;
KW plant pathogenesis-related protein.
XX
OS synthetic.
XX
PN EP392225-A.
XX
PD 17-OCT-1990.
XX
PF 21-MAR-1990; 90EP-0105336.
XX

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PR 20-OCT-1989; 89US-0425504.
PR 24-MAR-1989; 89US-0329018.
PR 20-JUN-1989; 89US-0368672.
XX
XX
PA (CIBA ) CIBA GEIGY AG.
XX
PI Ryals JA, Alexander DC, Goodman RM, Meins F, Payne GB;
PI Stinson JR, Neuhaus J-M, Moyer MB;
DR WPI. 1990-313983/42.
DR N-PSDB: AAQ06182.
XX
XX Disease-resistant transgenic plants - obtd. using encoding an
PT inducible pathogenesis-related protein from infected plants.
XX
XX Example 15, page 22; 77pp; English.
XX
XX This is the plant pathogenesis-related protein (PRP), PR-1c. It
CC confers systemic acquired resistance to plants. The corresp. DNA
CC is used, in a chimeric construct, to produce transgenic plant cells
CC or -tissues with the ability to regenerate into plants which are
CC disease resistant.
XX See also AAQ06179-81, AAQ06183-86 and AAQ06199-006208.
SQ Sequence 138 AA;

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Query Match 27.3%; Score 296; DB 11; Length 138;
Best Local Similarity 44.3%; Pred. No. 8.1e-20;
Matches 62; Conservative 15; Mismatches 51; Indels 12; Gaps 3;

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DB 59 WSGDGLTAARAKAVEMVVEKQYAHDSNTCAQGVCGHYTQVWRNSVVGARVQCUNNG 118

QY 184 ATTLCLYNPHGNVGOOSPY 203
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DB 119 GYIVSCNDPFGNVYGRSPY 138

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Job time : 38 secs





GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 19, 2003, 09:35:38 ; Search time 15 Seconds  
(without alignments) 398.190 Million cell updates/sec

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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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| 1          | 331   | 30.5        | 163    | 4  | US-09-257-583-13<br>Sequence 13, Appl   |
| 2          | 303   | 27.9        | 139    | 2  | US-07-857-224B-102<br>Sequence 102, App |
| 3          | 299   | 27.6        | 141    | 2  | US-07-857-224B-104<br>Sequence 104, App |
| 4          | 296   | 27.3        | 138    | 2  | US-07-857-224B-100<br>Sequence 100, App |
| 5          | 286   | 26.4        | 168    | 1  | US-08-181-271A-45<br>Sequence 45, Appl  |
| 6          | 286   | 26.4        | 168    | 1  | US-08-449-315-45<br>Sequence 45, Appl   |
| 7          | 286   | 26.4        | 168    | 1  | US-08-444-803-45<br>Sequence 45, Appl   |
| 8          | 286   | 26.4        | 168    | 1  | US-08-449-043-45<br>Sequence 45, Appl   |
| 9          | 286   | 26.4        | 168    | 1  | US-08-456-265A-45<br>Sequence 45, Appl  |
| 10         | 286   | 26.4        | 168    | 1  | US-08-455-416-45<br>Sequence 45, Appl   |
| 11         | 286   | 26.4        | 168    | 1  | US-08-455-244-45<br>Sequence 45, Appl   |
| 12         | 286   | 26.4        | 168    | 1  | US-08-454-876-45<br>Sequence 45, Appl   |
| 13         | 286   | 26.4        | 168    | 1  | US-08-457-364-45<br>Sequence 45, Appl   |
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| 15         | 286   | 26.4        | 168    | 2  | US-08-456-240-45<br>Sequence 45, Appl   |
| 16         | 286   | 26.4        | 168    | 2  | US-08-455-736-45<br>Sequence 45, Appl   |
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| 20         | 283.5 | 26.1        | 167    | 3  | US-08-773-368-5<br>Sequence 5, Appl     |
| 21         | 283.5 | 26.1        | 171    | 3  | US-09-199-887-5<br>Sequence 6, Appl     |
| 22         | 283   | 26.1        | 171    | 3  | US-09-199-887-6<br>Sequence 6, Appl     |
| 23         | 283   | 26.1        | 171    | 3  | US-07-857-224B-99<br>Sequence 99, Appl  |
| 24         | 281.5 | 25.9        | 135    | 2  | US-07-857-224B-97<br>Sequence 97, Appl  |
| 25         | 278.5 | 25.7        | 135    | 2  | US-07-857-224B-98<br>Sequence 98, Appl  |
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| 43 | 235   | 21.7 | 114 | 2 | US-07-857-224B-107<br>Sequence 107, App |
| 44 | 228   | 21.0 | 114 | 2 | US-07-857-224B-108<br>Sequence 108, App |
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## ALIGNMENTS

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; Patent No. 6429362
; GENERAL INFORMATION:
; APPLICANT: Crane, Virginia
; TITLE OF INVENTION: Family Of Maize PR-1 Genes And Promoters
; FILE REFERENCE: 5718-32, 035718/175219
; CURRENT APPLICATION NUMBER: US/09/257,583A
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Zea mays
US-09-257-583-13

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QY 197 VQGOSPY 203
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DB 157 VVGESPY 163

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; Sequence 102, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures Of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlaubstrasse 151
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: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Macintosh 7.0
: SOFTWARE: Microsoft Word
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/857,224B
: FILING DATE: 03/25/92
: CLASSIFICATION: 436
: PRIOR APPLICATION DATA:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (International) 41 1 632 2830
: TELEFAX: (International) 41 1 262 2437
:
: INFORMATION FOR SEQ ID NO: 100:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 138
: TYPE: amino acid
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
: DESCRIPTION: protein
: ORIGINAL SOURCE:
: FEATURE: Pathogenesis related protein; Table 16 Row 4
: PUBLICATION INFORMATION:
: AUTHORS:
: AUTHORS: Cutt, J. R.
: AUTHORS: Dixon, D. C.
: AUTHORS: Carr, J. P.
: AUTHORS: Klessig, D. F.
: TITLE: Isolation and nucleotide sequence of cDNA clones for the
: TITLE: Pathogenesis related proteins of Nicotiana tabacum induced by TMV
: TITLE: Infection.
: JOURNAL: Nucleic Acids Research
: VOLUME: 16
: PAGES: 9861
: DATE: 1988
:
: US-07-857-224B-100
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: Query Match 27.3%; Score 296; DB 2; Length 138;
: Best Local Similarity 44.3%; Pred. No. 1.8e-23;
: Matches 62; Conservative 15; Mismatches 51; Indels 12; Gaps 3;
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: Oy 125 WASYR-ARPAEYVALWYAEGRYTTNANTTCAGRQGGTTOYVWNTAEVGCACASCATG 183
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: Oy 184 ATLFLCYLPHNGVNGOSPY 203
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: RESULT 5
: US-08-181-271A-45
: Sequence 45, Application US/08181271A
: Patent No. 5614395
:
: GENERAL INFORMATION:
: APPLICANT: Ryals, John A.
: APPLICANT: Alexander, Danny C.
: APPLICANT: Beck, James J.
: APPLICANT: Duesing, John H.
: APPLICANT: Friedrich, Leslie B.
: APPLICANT: Goodman, Robert M.
: APPLICANT: Harms, Christian
: APPLICANT: Meins, Jr., Frederick
: APPLICANT: Montoya, Alice
: APPLICANT: Moyer, Mary B.
: APPLICANT: Neuhaus, Jean-Marc
: APPLICANT: Payne, George B.
```

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: APPLICANT: Sperison, Christoph
: APPLICANT: Stinson, Jeffrey R.
: APPLICANT: Uknes, Scott J.
: APPLICANT: Ward, Eric R.
: APPLICANT: Williams, Shericca C.
: TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
: TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
: NUMBER OF SEQUENCES: 106
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CIBA-GEIGY Corporation
: STREET: 7 Skyline Drive
: CITY: Hawthorne
: STATE: New York
: COUNTRY: USA
: ZIP: 10532
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/181,271A
: FILING DATE: 13-JAN-94
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/093,301
: FILING DATE: 16-JUL-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/937,197
: FILING DATE: 6-NOV-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/678,378
: FILING DATE: 1-APR-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/305,566
: FILING DATE: 6-FEB-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/165,667
: FILING DATE: 8-MAR-1988
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/042,847
: FILING DATE: 6-APR-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/632,441
: FILING DATE: 21-DEC-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/425,504
: FILING DATE: 20-OCT-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/848,506
: FILING DATE: 6-MAR-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/768,122
: FILING DATE: 27-SEP-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/580,431
: FILING DATE: 7-SEP-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/368,672
: FILING DATE: 20-JUN-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/329,018
: FILING DATE: 24-MAR-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/045,957
: FILING DATE: 12-APR-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Elmer, James Scott
: REGISTRATION NUMBER: 36,129
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919)541-8614
: TELEFAX: (919)541-8689
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: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 168 amino acids
:   TYPE: amino acid
:   TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-181-271A-45

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Matches 69; Conservative 22; Mismatches 59; Indels 38; Gaps 7;

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Db 13 LLVSTLLFLVI---SHSCR-----AONSQO-----DYLDHNTARADV 48
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OY 82 GVAFLRNAGLASAAGTVAQORROGCAFDVGA----SPYGAN--OGMASYRARAAY 135
   ||:||||| :|| :|||
Db 49 GVEPLTWDDQVAVAQNVASQ-----LAADCNLVHSHGQYGENLAEGSDFT-AKA 100
   ||:||||| :|| :|||
OY 136 VALVWAGRYTHANNTCAGROCGTYTQVWRNTAEVCAQASCATGATLTCLYHPHG 195
   ||:||||| :|| :|||
Db 101 VEMWVDEKQYYDHSNTCAQGVCGHYTQVWRNSVRVCARVCCNNGVYVSCNDPVG 160
   ||:||||| :|| :|||
OY 196 NVQOSPEY 203
   ||:|||||
Db 161 NYNGESPY 168

RESULT 6
US-08-449-315-45
: Sequence 45, Application US/08449315
: Patent No. 5650505
: GENERAL INFORMATION:
: APPLICANT: Ryals, John A.
: APPLICANT: Alexander, Danny C.
: APPLICANT: Beck, James J.
: APPLICANT: Duesling, John H.
: APPLICANT: Friedlich, Leslie B.
: APPLICANT: Goodman, Robert M.
: APPLICANT: Harms, Christian
: APPLICANT: Meins, Jr., Frederick
: APPLICANT: Montoya, Alice
: APPLICANT: Moyer, Mary B.
: APPLICANT: Neuhaus, Jean-Marc
: APPLICANT: Payne, George B.
: APPLICANT: Sperison, Christoph
: APPLICANT: Stinson, Jeffrey R.
: APPLICANT: Uknes, Scott J.
: APPLICANT: Ward, Eric R.
: APPLICANT: Williams, Shericea C.
: TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
: TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
: NUMBER OF SEQUENCES: 106
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: CIBA-GEIGY Corporation
: STREET: 7 Skyline Drive
: City: Hawthorne
: STATE: New York
: COUNTRY: USA
: ZIP: 10532
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/449,315
: FILING DATE: 24-MAY-1995
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/181,271
: FILING DATE: 13-JAN-94
:
: APPLICATION NUMBER: US 08/093,301
: FILING DATE: 16-JUL-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/937,197
: FILING DATE: 6-NOV-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/678,378
: FILING DATE: 1-APR-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/305,566
: FILING DATE: 6-FEB-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/165,667
: FILING DATE: 8-MAR-1988
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/042,847
: FILING DATE: 6-APR-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/632,441
: FILING DATE: 21-DEC-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/425,504
: FILING DATE: 20-OCT-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/848,506
: FILING DATE: 6-MAR-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/768,122
: FILING DATE: 27-SEP-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/580,431
: FILING DATE: 7-SEP-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/368,672
: FILING DATE: 20-JUN-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/329,018
: FILING DATE: 24-MAR-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/045,957
: FILING DATE: 12-APR-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Elmer, James Scott
: REGISTRATION NUMBER: 36,129
: REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919)541-8614
: TELEFAX: (919)541-8689
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 168 amino acids
:   TYPE: amino acid
:   TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-449-315-45

Query Match
Best Local Similarity 26.4%; Score 286; DB 1; Length 168;
Matches 69; Conservative 22; Mismatches 59; Indels 38; Gaps 7;

OY 22 LLATLALCAAPAPTHGARVLMFGAGAVTKAQQGGTSSGNATADETLAPHNOARAV 81
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Db 13 LLVSTLLFLVI---SHSCR-----AONSQO-----DYLDHNTARADV 48
   ||:||||| :|| :|||
OY 82 GVAFLRNAGLASAAGTVAQORROGCAFDVGA----SPYGAN--OGMASYRARAAY 135
   ||:||||| :|| :|||
Db 49 GVEPLTWDDQVAVAQNVASQ-----LAADCNLVHSHGQYGENLAEGSDFT-AKA 100
   ||:||||| :|| :|||
OY 136 VALVWAGRYTHANNTCAGROCGTYTQVWRNTAEVCAQASCATGATLTCLYHPHG 195
   ||:||||| :|| :|||
Db 101 VEMWVDEKQYYDHSNTCAQGVCGHYTQVWRNSVRVCARVCCNNGVYVSCNDPVG 160
   ||:||||| :|| :|||
OY 196 NVQOSPEY 203
```



APPLICANT: Williams, Shericca C.  
 TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
 TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
 NUMBER OF SEQUENCES: 106  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: CIBA-GEIGY Corporation  
 STREET: 7 Skyline Drive  
 CITY: Hawthorne  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10532  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/449,043  
 FILING DATE: 24-MAY-1995  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/181,271  
 FILING DATE: 13-JAN-94  
 APPLICATION NUMBER: US 08/093,301  
 FILING DATE: 16-JUL-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/937,197  
 FILING DATE: 6-NOV-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/678,378  
 FILING DATE: 1-APR-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/305,566  
 FILING DATE: 6-FEB-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/165,667  
 FILING DATE: 8-MAR-1988  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/042,847  
 FILING DATE: 6-APR-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/632,441  
 FILING DATE: 21-DEC-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/425,504  
 FILING DATE: 20-OCT 1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/848,506  
 FILING DATE: 6-MAR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/768,122  
 FILING DATE: 27-SEP-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/580,431  
 FILING DATE: 7-SEP-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/368,672  
 FILING DATE: 20-JUN-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/329,018  
 FILING DATE: 24-MAR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/045,957  
 FILING DATE: 12-APR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Elmet, James Scott  
 REGISTRATION NUMBER: 36,129  
 REFERENCE/DOCKET NUMBER: S-19925/P1/CGC 1727  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (919)541-8614  
 TELEFAX: (919)541-8689  
 INFORMATION FOR SEQ ID NO: 45:  
 SEQUENCE CHARACTERISTICS:

LENGTH: 168 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-449-043-45  
 Query Match 26.4%; Score 286; DB 1; Length 168;  
 Best local similarity 36.7%; Pred. No. 2.6e-22;  
 Matches 69; Conservative 22; Mismatches 59; Indels 38; Gaps 7;  
 QY 22 LILATLALCAPAPRPHGARVLMFGAGAVYKAAQGGTSGSGSNATDEYLAIPHNRARAV 81  
 DB 13 LVLSTLLFLVLT--SHSCR-----AQN500-----DYDAHNTARADV 48  
 QY 82 GVALRNMNGLASAAAGTVAQQRQGGCAFDVGA---SPYGAN--QGWASYRARPAY 135  
 DB 49 GVEPLTWMDQVAAYVQNNVASQ-----LAADCNLVHSHGOYGENLAEGSGDFMT-AAKA 100  
 QY 136 VALTVAEGRYTHANNTCAGRCQCTTYQVYRRTAVGCAQASCATGATLTLCYNPHG 195  
 DB 101 VEMWVDEKQYDHSNTCAQGVCGHYTVVWRMSVRVGCARVQCANNNGTYVSCNTDPG 160  
 QY 196 NVOGQSPY 203  
 DB 161 NVRGESPY 168  
 RESULT 9  
 US-08-456-265A-45  
 Sequence 45, Application US/08456265A  
 Patent No. 5767369  
 GENERAL INFORMATION:  
 APPLICANT: Alexander, Danny C.  
 APPLICANT: Ryals, John A.  
 APPLICANT: Goodman, Robert M.  
 APPLICANT: Stinson, Jeffrey R.  
 TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
 TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
 NUMBER OF SEQUENCES: 111  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CIBA-GEIGY Corporation  
 STREET: 520 White Plains Road, P.O. Box 2005  
 CITY: Tarrytown  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10591  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/456,265A  
 FILING DATE: 31-MAY-95  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/181,271  
 FILING DATE: 13-JAN-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/093,301  
 FILING DATE: 16-JUL-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/937,197  
 FILING DATE: 6-NOV-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/678,378  
 FILING DATE: 1-APR-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/305,566  
 FILING DATE: 6-FEB-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/165,667  
 FILING DATE: 8-MAR-1988

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PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38, 241
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ. ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-455-265A-45

Query Match 26.4%; Score 286; DB 1; Length 168;
Best Local Similarity 36.7%; Pred. No. 2,6e-22;
Matches 69; Conservative 22; Mismatches 59; Indels 38; Gaps 7

QY 22 LLLATLLALCAAPFTHGARYLMPGAGAYTKAQQGGTSGSNATDELTAAPHQARAV 81
Db 13 LLLVLTLLLELYT---SISCR-----ADNSOO-----DILDHNTNRADV 48
QY 82 GVAFLRMWAGLASAAGTVAQAQRQGGCAFDVGA---SPYGAN--QGMASRYRPAEV 135
Db 49 GVEPLTWDDQVAAAYNAONYASQ-----LAADCNLVSHQYGENIAEGSGDFMT-AAKA 100
QY 136 VALWAEGRYYTHANNTCAGAGRCGGTYGYWWRNTAEVGAQASCATGATLTLCYDPHG 195
Db 101 VEMWVDEQGYHDHNSNTCAAGQGVCGHYGYWWRNSYVGCARQCANNNGYVSCNIDPPG 160
QY 196 NWQGGSPY 203
Db 161 NRGESPY 168

RESULT 10
US-08-455-416-45
: Sequence 45, Application US/08455416
: Patent No. 5777200
: GENERAL INFORMATION:
: APPLICANT: Ryals, John A.
: APPLICANT: Alexander, Danny C.
: APPLICANT: Beck, James J.
: APPLICANT: Fiedrich, John H.
: APPLICANT: Fiedrich, Leslie B.

```

APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
TITLE OF INVENTION: Williams, Sherilca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,416  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible

Db

|    |    |              |       |       |       |       |            |    |
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|    | 26 | LIVSTELLFVIT | SHSCR | ----- | AQNSQ | ----- | DYLAHNTADV | 48 |
| G7 | 26 | LIVSTELLFVIT | SHSCR | ----- | AQNSQ | ----- | DYLAHNTADV | 48 |



|    |     |   |       |                             |   |              |     |
|----|-----|---|-------|-----------------------------|---|--------------|-----|
| QY | 82  | GVAPELRNNGNLAAAGVTAOORRGGCAFDVDA                          | ----  | SPGAN                       | - | GGMSYARAPREV | 135 |
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| Db | 49  | GVEPELTMDQDQVAAYNQNTASQ                                   | ----- | LAADCNLVHSHGQYGENLAEDSDQFMT | - | AKA          | 100 |
|    |     | :   :   |       |                             |   |              |     |
| QY | 136 | VALVAEAGSYTHHANTCAAGROGCTGYVWYRNTAEVCAQASCATGATLTLLLYPHG  | 135   |                             |   |              |     |
|    |     | :   :   |       |                             |   |              |     |
| Db | 101 | VEKMWDEKQYTHDSDNTCAQGGCGHTTYWWRNSRVAGCAKQCINNGSYVSCNTIDPG | 160   |                             |   |              |     |
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| QY | 196 | NVOGQSPY  | 203   |                             |   |              |     |
|    |     | :   :   |       |                             |   |              |     |
| Db | 161 | NYRGESPY  | 168   |                             |   |              |     |
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1 RESULT 12
2 US-08-454-876-45
3 Sequence 45, Application US/08454876
4 Patent No. 5804593
5
6 GENERAL INFORMATION:
7
8 APPLICANT: Ryals, John A.
9 APPLICANT: Alexander, Danny C.
10 APPLICANT: Beck, James J.
11 APPLICANT: Duesing, John H.
12 APPLICANT: Friedrich, Leslie B.
13 APPLICANT: Goodman, Robert M.
14 APPLICANT: Harms, Christian
15 APPLICANT: Meins, Jr., Frederick
16 APPLICANT: Montoya, Alice
17 APPLICANT: Moyer, Mary B.
18 APPLICANT: Neuhaus, Jean-Marc
19 APPLICANT: Payne, George B.
20 APPLICANT: Sperison, Christoph
21 APPLICANT: Stinson, Jeffrey R.
22 APPLICANT: Uknes, Scott J.
23 APPLICANT: Ward, Eric R.
24
25 TITLE OF INVENTION: CHEMICAL REGULATABLE AND ANTI-PATHOGENIC
26 TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
27 NUMBER OF SEQUENCES: 106
28
29 CORRESPONDENCE ADDRESS:
30 ADDRESSEE: CIBA-GEIGY Corporation
31 STREET: 7 Skyline Drive
32 CITY: Hawthorne
33 STATE: New York
34 COUNTRY: USA
35 ZIP: 10532
36
37 COMPUTER READABLE FORM:
38 MEDIUM TYPE: Floppy disk
39 OPERATING SYSTEM: IBM PC compatible
40 SOFTWARE: Patentln Release #1.0, Version #1.25
41
42 CURRENT APPLICATION DATA:
43 APPLICATION NUMBER: US/08/454,876
44 FILING DATE: 31-MAY-1995
45 CLASSIFICATION: 435
46
47 PRIOR APPLICATION DATA:
48 APPLICATION NUMBER: 08/181,271
49 FILING DATE: 13-JAN-94
50 APPLICATION NUMBER: US 08/093,301
51 FILING DATE: 16-JUL-1993
52
53 PRIOR APPLICATION DATA:
54 APPLICATION NUMBER: US 07/937,197
55 FILING DATE: 6-NOV-1992
56
57 PRIOR APPLICATION DATA:
58 APPLICATION NUMBER: US 07/678,378
59 FILING DATE: 1-APR-1991
60
61 PRIOR APPLICATION DATA:
62 APPLICATION NUMBER: US 07/305,566
63 FILING DATE: 6-FEB-1989
64
65 PRIOR APPLICATION DATA:
66 APPLICATION NUMBER: US 07/165,667
67 FILING DATE: 8-MAR-1988
68
69 PRIOR APPLICATION DATA:
70 APPLICATION NUMBER: US 08/042,847
71
72

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1      FLING DATE: 6-APR-1993
2      PRIOR APPLICATION DATA:
3      APPLICATION NUMBER: US 07/652,441
4      FLING DATE: 21-DEC-1990
5      PRIOR APPLICATION DATA:
6      APPLICATION NUMBER: US 07/425,504
7      FLING DATE: 20-OCT 1989
8      PRIOR APPLICATION DATA:
9      APPLICATION NUMBER: US 07/848,506
10     FLING DATE: 6-MAR-1992
11     PRIOR APPLICATION DATA:
12     APPLICATION NUMBER: US 07/768,122
13     FLING DATE: 27-SEP-1991
14     PRIOR APPLICATION DATA:
15     APPLICATION NUMBER: US 07/580,431
16     FLING DATE: 7-SEP-1990
17     PRIOR APPLICATION DATA:
18     APPLICATION NUMBER: US 07/368,672
19     FLING DATE: 20-JUN-1989
20     PRIOR APPLICATION DATA:
21     APPLICATION NUMBER: US 07/329,018
22     FLING DATE: 24-MAR-1989
23     PRIOR APPLICATION DATA:
24     APPLICATION NUMBER: US 08/045,957
25     FLING DATE: 12-APR-1993
26     ATTORNEY/AGENT INFORMATION:
27     NAME: Elmer James Scott
28     REGISTRATION NUMBER: 36,129
29     REFERENCE/DOCKET NUMBER: S-19825/P1/CSC 1727
30     TELECOMMUNICATION INFORMATION:
31     TELEPHONE: (919)541-8614
32     TELEFAX: (919)541-8689
33     INFORMATION FOR SEQ ID NO: 45:
34     SEQUENCE CHARACTERISTICS:
35     LENGTH: 168 amino acids
36     TYPE: amino acid
37     TOPOLOGY: linear
38     MOLECULE TYPE: protein
39     OS-08-454-876-45

```

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Query Match          26.4% ; Score 286; DB 1; Length 168;
Best Local Similarity 36.7% ; Pred No. 2.6e-22;
Matches 69; Conservative 22; Mismatches 59; Indels 38; Gaps 7

QY      22  LLATLTLALCAAPAPTHGARVIMPGAGAVTKAQQGGTSGSNATADEYLAIPHNAARAAV 81
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DB      13  LLVSTLTLFLVIT--SHSCR-----AQNQQ-----DYLDHHTARADV 48
      |||::|||      :|      :||

QY      82  GVALPRLRNAGLAGAAGTVAQQDRQGGCAFADYGA-----SPRYGAN--QGMASTYARAEV 135
      |||::|||      :|      :||
DB      49  GVEPLATWDDOVAAYAONTVASQ-----LAQDCNLVHSHGQYIGENLAEGSGDEFTT-AAKA 100
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QY      136 VALVWAGRGYYTTHANNNTCAAGRCQGYTQVWRNRTAEYGAQAQASCATGATLLTLYNPHG 195
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DB      101 VEMWVDEKQYTHDHSNTCAQGGVCGHYTQVWRNSVRYGCARVQCNNNGYGVSCNDVDPG 160
      :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      196 NVQGSQSPY 203
      |::|::|::|

DB      161 NYRGESPY 168

RESULT 13
US-08-457-364-45
; Sequence 45 Application US/08457364
; Patent No. 5847258
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian

```

APPLICANT: Meins, Jr., Frederick  
 APPLICANT: Montoya, Alice  
 APPLICANT: Moyer, Mary B.  
 APPLICANT: Neuhaus, Jean-Marc  
 APPLICANT: Payne, George B.  
 APPLICANT: Sperison, Christoph  
 APPLICANT: Stinson, Jeffrey R.  
 APPLICANT: Uknes, Scott J.  
 APPLICANT: Ward, Eric R.  
 APPLICANT: Williams, Shericoa C.  
 TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
 TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
 NUMBER OF SEQUENCES: 106  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CIBA-GEIGY Corporation  
 STREET: 7 Skyline Drive  
 CITY: Hawthorne  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10532  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/457,364  
 FILING DATE: 31-MAY-1995  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/181,271  
 FILING DATE: 13-JAN-94  
 APPLICATION NUMBER: US 08/093,301  
 FILING DATE: 16-JUL-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/937,197  
 FILING DATE: 6-NOV-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/678,378  
 FILING DATE: 1-APR-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/305,566  
 FILING DATE: 6-FEB-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/165,667  
 FILING DATE: 8-MAR-1988  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/042,847  
 FILING DATE: 6-APR-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/632,441  
 FILING DATE: 21-DEC-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/425,504  
 FILING DATE: 20-OCT-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/848,506  
 FILING DATE: 6-MAR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/768,122  
 FILING DATE: 27-SEP-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/580,431  
 FILING DATE: 7-SEP-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/368,672  
 FILING DATE: 20-JUN-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/329,018  
 FILING DATE: 24-MAR-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/045,957  
 FILING DATE: 12-APR-1993

ATTORNEY/AGENT INFORMATION:  
 NAME: Elmer, James Scott  
 REGISTRATION NUMBER: 36,129  
 REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (919)541-8614  
 TELEFAX: (919)541-8689  
 INFORMATION FOR SEQ ID NO: 45:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 168 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
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 DB 49 GVEPLTWDDQVAAVAQNTVASQ-----LAADCNLVSHSGYGENVILABSGSDPMT-AAKA 100  
 QY 136 VALVAEGRYTHANNTCAGACGCGTYTOYVWNRNTAEVGCACASCATGATLTLCLYNPHG 195  
 DB 101 VEMVWDEKQYHDNSTCAQGOVCGHYTOYVWNRNVGACARQCNGSYVSCNYDPG 160  
 QY 196 NVQGSQSPY 203  
 DB 161 NYRGESPY 168  
 RESULT 14  
 US-08-456-262-45  
 Sequence 45, Application US/08456262  
 Patent No. 5851766  
 GENERAL INFORMATION:  
 APPLICANT: Ryals, John A.  
 APPLICANT: Alexander, Danny C.  
 APPLICANT: Beck, James J.  
 APPLICANT: Duesling, John H.  
 APPLICANT: Friedrich, Leslie B.  
 APPLICANT: Goodman, Robert M.  
 APPLICANT: Harms, Christian  
 APPLICANT: Meins, Jr., Frederick  
 APPLICANT: Montoya, Alice  
 APPLICANT: Moyer, Mary B.  
 APPLICANT: Neuhaus, Jean-Marc  
 APPLICANT: Payne, George B.  
 APPLICANT: Sperison, Christoph  
 APPLICANT: Stinson, Jeffrey R.  
 APPLICANT: Uknes, Scott J.  
 APPLICANT: Ward, Eric R.  
 APPLICANT: Williams, Shericoa C.  
 TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
 TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
 NUMBER OF SEQUENCES: 106  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CIBA-GEIGY Corporation  
 STREET: 7 Skyline Drive  
 CITY: Hawthorne  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10532  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25





GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: March 19, 2003, 09:37:17 ; Search time 16 Seconds

(without alignments)  
678.302 Million cell updates/sec

Title: US-09-832-320-2

Perfect score: 1085

Sequence: 1 MAHSRSHHLLLPAPMATA.....ATTLCLYNPHGNVQGSPPY 203

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 221153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_AA:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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| 1          | 1085  | 100.0       | 203    | 10 US-09-832-320-2   | Sequence 2, Appl1  |
| 2          | 331   | 30.5        | 163    | 10 US-09-840-479-13  | Sequence 13, Appl1 |
| 3          | 331   | 30.5        | 163    | 12 US-10-078-929-202 | Sequence 202, App  |
| 4          | 300.5 | 27.7        | 171    | 9 US-10-068-347-4    | Sequence 4, Appl1  |
| 5          | 287   | 26.5        | 164    | 12 US-10-078-929-82  | Sequence 82, Appl1 |
| 6          | 287   | 26.5        | 176    | 12 US-10-078-929-86  | Sequence 86, Appl1 |
| 7          | 280.5 | 25.9        | 167    | 12 US-10-078-929-100 | Sequence 100, App  |
| 8          | 267   | 24.6        | 136    | 9 US-10-091-135-83   | Sequence 83, Appl1 |
| 9          | 259.5 | 23.9        | 164    | 12 US-10-078-929-84  | Sequence 84, Appl1 |
| 10         | 255   | 23.5        | 161    | 12 US-10-078-929-96  | Sequence 96, Appl1 |
| 11         | 254   | 23.4        | 190    | 12 US-10-078-929-90  | Sequence 90, Appl1 |
| 12         | 248   | 22.9        | 139    | 12 US-10-078-929-94  | Sequence 94, Appl1 |
| 13         | 240   | 22.1        | 156    | 10 US-09-840-479-7   | Sequence 7, Appl1  |
| 14         | 231   | 21.3        | 156    | 12 US-10-078-929-98  | Sequence 98, Appl1 |
| 15         | 223.5 | 20.6        | 94     | 9 US-10-068-347-2    | Sequence 2, Appl1  |
| 16         | 223.5 | 20.6        | 214    | 10 US-09-840-479-15  | Sequence 15, Appl1 |
| 17         | 217.5 | 20.0        | 112    | 12 US-10-078-929-88  | Sequence 88, Appl1 |
| 18         | 199   | 18.3        | 112    | 12 US-10-078-929-92  | Sequence 92, Appl1 |
| 19         | 197   | 18.2        | 140    | 12 US-10-078-929-92  | Sequence 92, Appl1 |

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| 20 | 193.5 | 17.8 | 455 | 9 US-09-944-413-50   | Sequence 50, Appl1 |
| 21 | 193.5 | 17.8 | 455 | 9 US-09-944-403-50   | Sequence 50, Appl1 |
| 22 | 193.5 | 17.8 | 455 | 9 US-09-944-896-50   | Sequence 50, Appl1 |
| 23 | 193.5 | 17.8 | 455 | 9 US-09-944-944-50   | Sequence 50, Appl1 |
| 24 | 193.5 | 17.8 | 455 | 9 US-09-944-907-50   | Sequence 50, Appl1 |
| 25 | 193.5 | 17.8 | 455 | 9 US-09-944-929-50   | Sequence 50, Appl1 |
| 26 | 193.5 | 17.8 | 455 | 10 US-09-866-028-50  | Sequence 50, Appl1 |
| 27 | 193.5 | 17.8 | 455 | 10 US-09-944-449-50  | Sequence 50, Appl1 |
| 28 | 193.5 | 17.8 | 455 | 10 US-09-944-457-50  | Sequence 50, Appl1 |
| 29 | 193.5 | 17.8 | 455 | 10 US-09-944-862-50  | Sequence 50, Appl1 |
| 30 | 193.5 | 17.8 | 455 | 10 US-09-945-587-50  | Sequence 50, Appl1 |
| 31 | 193.5 | 17.8 | 455 | 10 US-09-945-015-50  | Sequence 50, Appl1 |
| 32 | 193.5 | 17.8 | 455 | 10 US-09-944-396-50  | Sequence 50, Appl1 |
| 33 | 193.5 | 17.8 | 455 | 10 US-09-944-097-50  | Sequence 50, Appl1 |
| 34 | 193.5 | 17.8 | 455 | 10 US-09-944-432-50  | Sequence 50, Appl1 |
| 35 | 193.5 | 17.8 | 455 | 10 US-09-943-762-50  | Sequence 50, Appl1 |
| 36 | 193.5 | 17.8 | 455 | 10 US-09-944-654-50  | Sequence 50, Appl1 |
| 37 | 193.5 | 17.8 | 455 | 10 US-09-944-654-50  | Sequence 50, Appl1 |
| 38 | 189.5 | 17.5 | 109 | 12 US-10-078-929-208 | Sequence 208, App  |
| 39 | 188.5 | 17.4 | 446 | 9 US-10-042-141-47   | Sequence 47, Appl1 |
| 40 | 188.5 | 17.4 | 446 | 10 US-09-726-643-47  | Sequence 47, Appl1 |
| 41 | 188.5 | 17.4 | 446 | 10 US-09-790-264-2   | Sequence 2, Appl1  |
| 42 | 179   | 16.5 | 420 | 10 US-09-790-264-4   | Sequence 4, Appl1  |
| 43 | 177   | 16.3 | 463 | 9 US-09-905-291A-285 | Sequence 285, App  |
| 44 | 177   | 16.3 | 463 | 9 US-09-902-853-285  | Sequence 285, App  |
| 45 | 177   | 16.3 | 463 | 9 US-09-907-824-285  | Sequence 285, App  |

## ALIGNMENTS

RESULT 1  
US-09-832-320-2  
; Sequence 2, Application US/09832320  
; Patent No. US20010049834A1  
; GENERAL INFORMATION:  
; APPLICANT: Crane, Edmund H.  
; TITLE OF INVENTION: Maize Pathogenesis-Related  
; FILE REFERENCE: 35718/214291  
; CURRENT APPLICATION NUMBER: US/09/832,320  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: US 60/195,801  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 203  
; TYPE: PRT  
; ORGANISM: Zea mays  
US-09-832-320-2

Query Match 100.0%; Score 1085; DB 10; Length 203;  
Best Local Similarity 100.0%; Pred. No. 5.5e-85;  
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| QY | 61  | SGSNATADETLAPHNQARA |  | VGAPLRWNAGLSAAGTVAAQORGGCAFPDVGASPTG     | 120 |
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| QY | 121 | ANOGWASYRAPPAEVAL   |  | WALWAEGRYTHANNITCAAGROGTYVWVRMTAEVGAQASC | 180 |
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; Sequence 13, Application US/09840479
; Patent No. US2001002580A1
; GENERAL INFORMATION:
; APPLICANT: Crane, Virginia
; TITLE OF INVENTION: Family of Maize PR-1 Genes And Promoters
; FILE REFERENCE: 5718-32, 035718/175219
; CURRENT APPLICATION NUMBER: US/09/840,479
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/257,583
; PRIOR FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Zea mays
US-09-840-479-13

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Best Local Similarity 39.0%; Pred. No. 3.7e-21;
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QY 138 LMAVEGRYTYHANTTCAAGRCCTTYQVWVRNTAEVGCQAQASCATGA-TLTLCLYNPHGN 196
DB 97 SWSEKQYTDHTNSCAEGQVCGHYTYVWRDSTAIGCARVYCDNNAGVITICSYNPPGN 156

QY 197 VOGOSPY 203
DB 157 VVGESPY 163

RESULT 3
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; Sequence 202, Application US/10078929
; Patent No. US20020152497A1
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni
; APPLICANT: Maao, Guo-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
; FILE REFERENCE: BR1357 US NA
; CURRENT APPLICATION NUMBER: US/10/078,929
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/566,394
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/133038
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133042
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11

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; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 202
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Zea mays
US-10-078-929-202

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Best Local Similarity 39.0%; Pred. No. 3.7e-21;
Matches 73; Conservative 21; Mismatches 61; Indels 32; Gaps 6;

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DB 6 ACLALAMAATVAPC-----TAQNSPQD-YDPHNARA 39

QY 80 AVGAAPLRMNAAGLASAAGTVAQOROGCAFADVGASPYGANQWASYRA--RPAEYVA 137
DB 40 DVGVPVSMDDTVAAAYASQYAAQ--RQGDCLTHSG-GPYGENLFWSAGADMSASDAVG 96

QY 138 LMAVEGRYTYHANTTCAAGRCCTTYQVWVRNTAEVGCQAQASCATGA-TLTLCLYNPHGN 196
DB 97 SWSEKQYTDHTNSCAEGQVCGHYTYVWRDSTAIGCARVYCDNNAGVITICSYNPPGN 156

QY 197 VOGOSPY 203
DB 157 VVGESPY 163

RESULT 4
; US-10-068-347-4
; Sequence 4, Application US/10068347
; Patent No. US2002016616A1
; GENERAL INFORMATION:
; APPLICANT: Pioneer Hi-Bred International, Inc.
; APPLICANT: Acevedo, Pedro
; APPLICANT: Crane, Virginia
; TITLE OF INVENTION: Maize P1 Polynucleotides and Methods of Use
; FILE REFERENCE: 35718/242798 (5718-151)
; CURRENT APPLICATION NUMBER: US/10/068,347
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/267,052
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Zea mays
US-10-068-347-4

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Best Local Similarity 41.9%; Pred. No. 1.5e-18;
Matches 70; Conservative 17; Mismatches 63; Indels 17; Gaps 7;

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DB 17 VVAAAAGRVSAQN-----TAQDFVULHNSPADYGVGNVAMNTTVA-AYASQYA 66

QY 102 QOROGCAFADVGASPYGANQW--ASYRARAPEVVALMVAEGRYTYHANTTCAA--GR 157
DB 67 NQ-RAGDCRLVHSG-GPYGENLFWSAGVAMTASNAVGSMAAEKQYVNHATNTCSAPSGQ 124

QY 158 QCGITTYQVWVRNTAEVGCQAQASCATGA-TLTLCLYNPHGNVOGOSPY 203
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RESULT 5
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; Sequence 82, Application US/10078929
; Patent No. US20020152497A1
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; APPLICANT: Wang, Xude
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
; FILE REFERENCE: Bb137 US NA
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/566,394
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/133038
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133042
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 82
; LENGTH: 164
; TYPE: PR1
; ORGANISM: Zea mays
US-10-078-929-82

Query Match          26.5%; Score 287; DB 12; Length 164;
Best Local Similarity 39.9%; Fred. NO. 2e-17;
Matches 63; Conservative 23; Mismatches 66; Indels 6; Gaps 5.

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QY      167 WRNTAEYGCQAQASCATG-ATLTCLLYPHGVGOSPY 203
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DB      119 WRRSTRIGCARVVCADNRGVFTVCSDYDPGVNVNGORPF 156

RESULT 6
US-10-078-929-86
; Sequence 86, Application US/10078929
; Patent No. US20020152497A1
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime

```

```

1      APPLICANT: Famodu, Omolayo O.
2      APPLICANT: Odell, Joan T.
3      APPLICANT: Meyers, Blake
4      APPLICANT: Thorpe, Catherine
5      APPLICANT: Meng, Zude
6      TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved In
7      TITLE OF INVENTION: Stress Response
8      FILE REFERENCE: B1357 US NA
9      CURRENT APPLICATION NUMBER: US/10/078,929
1     PRIOR FILING DATE: 2002-02-19
11    PRIOR APPLICATION NUMBER: 09/566,394
12    PRIOR FILING DATE: 2000-05-05
13    PRIOR APPLICATION NUMBER: 60/133038
14    PRIOR FILING DATE: 1999-05-07
15    PRIOR APPLICATION NUMBER: 60/133042
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17    PRIOR APPLICATION NUMBER: 60/133427
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22    PRIOR FILING DATE: 1999-05-11
23    PRIOR APPLICATION NUMBER: 60/133438
24    PRIOR FILING DATE: 1999-05-11
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26    PRIOR FILING DATE: 1999-05-11
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31    SEQ ID NO 86
32    LENGTH: 176
33    TYPE: PRT
34    ORGANISM: Oryza sativa
35    US-10-078-929-86
36
37    Query Match          26.5%; Score 287; DB 12; Length 176;
38    Best Local Similarity 40.0%; Pred. NO. 2.2e-17;
39    Matches 70; Conservative 22; Mismatches 71; Indels 12; Gaps
40
41    QY 33 AAPFTHGARTLPGAGAAVTKAQQGGTSGSNATADEYLAPHNOAIRAVAPLRNAGI 92
42         ||| | | | | | | | | | | | | | | | | | | | | | | | | | | :
43    Db 2 APSKVSIAVL---VVAISLMAAATTTSQNPTPODVNLHNSARRADVGCVSWDPKV 57
44
45    QY 93 ASAAGVQAQQRQGACAFADGASGYGNGDMASY-RA-RPAVVVLWVAEGRYTTHAN 150
46         ||| | | | | | | | | | | | | | | | | | | | | | | | | | | :
47    Db 58 ASFQOSTAA--KKAQCRCRLQHSQ-GPYGENITFGSAGCAWSAADAAVASWGEKKNNHYDT 114
48
49    QY 151 NTCAGRGCGCTTYQVYVRNTAEYGAQMSCAT--GATLTCLLYPHGNVOGSDFY 203
50         ||| | | | | | | | | | | | | | | | | | | | | | | | | | | :
51    Db 115 NTCDPKGVCHYQVYWRKRSVRIGCARVCANRGTFT-CNYDPPGNFNGERPF 168
52
53 RESULT 7
54 US-10-078-929-100
55 Sequence 100, Application US/10078929
56 Patent No. US20020152497A1
57 GENERAL INFORMATION:
58 APPLICANT: Rafalski, Antoni
59 APPLICANT: Miao, Guo-Hua
60 APPLICANT: Falco, Saverio Carl
61 APPLICANT: Sakai, Hajime
62 APPLICANT: Famodu, Omolayo O.
63 APPLICANT: Ogelli, Joan T.
64 APPLICANT: Meyers, Blake
65 APPLICANT: Thorpe, Catherine
66 APPLICANT: Meng, Zude
67 TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved In
68 TITLE OF INVENTION: Stress Response
69 FILE REFERENCE: B1357 US NA
70 CURRENT APPLICATION NUMBER: US/10/078,929
71 CURRENT FILING DATE: 2002-02-19
72 PRIOR APPLICATION NUMBER: 09/566,394

```

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; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/133038
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133042
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 100
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-078-929-100

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Query Match 25.9%; Score 280.5; DB 12; Length 167;
Best Local Similarity 35.7%; Pred. No. 7.3e-17;
Matches 70; Conservative 26; Mismatches 61; Indels 39; Gaps 8;

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QY 15 APWATCCLLATLALCAAPAPTHGARVILMPGAGAVTKAQCSTGSGSNATDEVLAPH 74
DB 4 SPLSTVLLALASAM-----VVVTAN-----SPQDVEDH 35
QY 75 NQARAAGVAPLRMNAAGLASAAAGTVAAORRGGCAF----ADYGASPTANQMSSTRA 130
DB 36 NAARAVGVGPVWDNDNA-AVAQNYAEORR-GDCQLVHSGGQYGENITYRGSGADMTA 93
QY 131 RPAEVALVWAEGRYTHANNCA--AGROCGTYTVVWRNTAEVGAQASCATGATL-T 187
DB 94 --ADVQAVWSEKQYTDHGSNCSPADKSCHTGYVWRNSTLIGARVVCGGGGLFI 151
QY 188 LCLYNPHGNVQOSPY 203
DB 152 ICSYNPGEVGYSPY 167

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RESULT 8
US-10-091-135-83
; Sequence 83, Application US/10091135
; Publication No. US20030039660A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; APPLICANT: Spangfort, Michael Dho
; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
; FILE REFERENCE: 2313/14587-051
; CURRENT APPLICATION NUMBER: US/10/091,135
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/272,818
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Lycopersicon esculentum
US-10-091-135-83

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Query Match 24.6%; Score 267; DB 9; Length 136;
Best Local Similarity 44.2%; Pred. No. 8.2e-16;
Matches 61; Conservative 13; Mismatches 54; Indels 10; Gaps 5;
QY 69 EYLAPHNQAARAVGAPLRMNAAGLASAAAGTVAAORRGGCAFADYGASPTGAN--QGWA 126

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DB 6 DYLAIVNDARAQVGVGPMKMDANLASRAQNYA--NSRAGOCNLHSGA--GENLAKGGG 60
QY 127 SYARPAEYVALVWAEGRYTHANNCAAGROCGTYTVVWRNTAEVGAQASC-ATGAF 185
DB 61 DFTGRAA--VOLWVSERPSPYNATNQCVGKCRHRYTVVWRNSVRLGCGRACNNNGWA 118
QY 186 LTLCLYNPHGNVQOSPY 203
DB 119 FISCNTDPPVGNMIGORPY 136

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RESULT 9
US-10-078-929-84
; Sequence 84, Application US/10078929
; Patent No. US20020152497A1
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; APPLICANT: Meng, Zude
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
; FILE REFERENCE: BB1357 US NA
; CURRENT APPLICATION NUMBER: US/10/078,929
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/566,394
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/133038
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133042
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 84
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (22)
; NAME/KEY: UNSURE
; LOCATION: (50)
; NAME/KEY: UNSURE
; LOCATION: (56)
; NAME/KEY: UNSURE
; LOCATION: (59)
; NAME/KEY: UNSURE
; LOCATION: (99)
; NAME/KEY: UNSURE
; LOCATION: (121)
; NAME/KEY: UNSURE
; LOCATION: (140)
; NAME/KEY: UNSURE
; LOCATION: (150)
; NAME/KEY: UNSURE

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RESULT 12
US-10-078-929-94
; Sequence 94, Application US/10078929
; Patent No. US20020152497A1
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
; FILE REFERENCE: B31357 US NA
; CURRENT FILING DATE: 2002-02-19
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/133038
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133042
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 94
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Glycine max
US-10-078-929-94

Query Match          22.9%; Score 248; DB 12; Length 139;
Best Local Similarity 37.7%; Pred. No. 3.4e-14;
Matches 52; Conservative 21; Mismatches 61; Indels 4; Gaps 4;

QY 66 TADEYAPHNQARAAGVAPLRMNGIASAAAGTVAQORRGSCAFADVGASPYGANGW 125
DB 6 TPDELDVHNOARAAYGVGLPSMNTL-QATVAKRYANERIP-DCNL-EHSMGPGENLAE 62
QY 126 ASYRARPAAVVALWAEGRYTHANNCTCAAGROCGCTYOVVWRMTAEVGAQASCATGAT 185
DB 63 GYGEWGSDAVAFWLEKRYDYHYSNACVHD-ECLHTYQIWRSDSVHLGCARACNNDMW 121
QY 186 LITLCATNPHNGVOSQSPY 203
DB 122 FVICSTSPGNIEGKERPY 139

RESULT 13
US-09-840-479-7
; Sequence 7, Application US/09840479
; Patent No. US20010025380A1
; GENERAL INFORMATION:
; APPLICANT: Crane, Virginia
; TITLE OF INVENTION: Family Of Maize PR-1 Genes And Promoters
; FILE REFERENCE: 5718-32, 035718/175219
; CURRENT APPLICATION NUMBER: US/09/840,479
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/257,583
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PRIOR FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Zea mays
US-09-840-479-7

Query Match          22.1%; Score 240; DB 10; Length 156;
Best Local Similarity 44.5%; Pred. No. 1.9e-13;
Matches 53; Conservative 16; Mismatches 44; Indels 6; Gaps 4;

QY 69 EYLAPHNQARAAGVAPLRMNGIASAAAGTVAQORRGSCAFADVGASP--YGANGNA 126
DB 15 DEVNHNNAARAAGVGPVSDENVAFAFSYAAQ--RQGDCKLVHSGGPNHNGENIFWG 72
QY 127 SYRA-RPAEVVALWAEGRYTHANNCTCAAGROCGCTYOVVWRMTAEVGAQASCATGA 184
DB 73 GGSAMKASDAVGLWVGKONTDYNNSCAAGKVCGHYTOYVWRKSP-SAAPASSATTA 130

RESULT 14
US-10-078-929-98
; Sequence 98, Application US/10078929
; Patent No. US20020152497A1
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
; FILE REFERENCE: B31357 US NA
; CURRENT APPLICATION NUMBER: US/10/078,929
; CURRENT FILING DATE: 2002-02-19
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/133038
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133042
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 98
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Trifolium aestivum
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (107)..(108)..(109)..(110)
; NAME/KEY: UNSURE
; LOCATION: (137)
US-10-078-929-98

Query Match          22.1%; Score 240; DB 12; Length 156;
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Wed May 19 09:52:31 2003

us-09-832-320-2.rapp

Page 7

Best Local Similarity 38.68; Pred. NO. 1.9e-13;  
Matches 56; Conservative 22; Mismatches 47; Indels 20; Gaps 7.

Matches 56; Conservative 22; Mismatches 47; Indels 20; Gaps 7;

69 EYLAPHNQARA VGVAPLRWNAGLASAAGTVAQQRGGCAFADVGASPYGAN---QG 124

Db 22 DEVDPHNARADVGVPTWDDNVA-AYAQNVAEQR-GDCQLVHSGGQ-YGENITYGGRG 78

QY 125 WASYRARPAEVVALWVAEGRYTTHANNTCAGRCGGTYTQVVRNTAEVGAQA----- 178

Db 79 GADWTA--ADAVQAWSEKQYIDHGSNSCSXXXXCLHYTQVVRDSTGIGCARVVCDDGD 136

QY 179 SCATGATLTLCLYNPHGNVQGQSPY 203

Db 137 XCSSSAT-----NRATTKGVSPY 156

RESULT 15

US-10-068-347-2

Patent No. US20020166146A1

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;; GENERAL INFORMATION:
;; APPLICANT: Pioneer Hi-Bred Interna
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APPLICANT: Acevedo, Pedro

APPLICANT: Crane, Virginia

FILE REFERENCE: 35718/24279

CURRENT FILING DATE: 2002-

PRIOR FILING DATE: 2001-02-07

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; NUMBER OF SEQ ID NOS: 12
;
SOFTWARE: PatentIn version 3.0

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: SEQ ID NO 2
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: I. LENGTH: 166

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TYPE: PRT
OCCURANCE: FOR NEWS

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US-10-068-347-2

Query Match 21.38;

Best Local Similarity 35.0%;  
Matches 63; Conservative 1

46 GGAGGA

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DO NOT WRITE IN THESE SPACES

Query Match 21.3%; Score 231; DB 9; Length 166;

Best Local Similarity 33.06; Pred. No. 1.1e-12;  
Matches 63; Conservative 16; Mismatches 66; Indels 32; Gaps 8

46 GGAGAVTKAOGGTG-----SGSNATA-DEYIAPHNCAARAAGVAPI.RWNAGIASAA 96

[illegible]

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[illegible]

20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050

14/ THANNICAGROUSTYQVWNRNIAEVCAGASCATGATLTLCLYNPHGNVGGSPY 203

Db 110 HYSDSTCDPGRKMGHYKAVVWKTTSVGCGRICNSGDTIIMCSYWPNGNYHGKPY 166

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Search completed: March 19, 2003, 09:41:47
Job time : 17 secs
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GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model  
Run On: February 22, 2003, 04:06:26 ; Search time 44.5828 Seconds  
(without alignments)  
4209.836 Million cell updates/sec

Title: US-09-832-320-3  
Perfect score: 612  
Sequence: 1 atggcgactcgcgcagcca.....agggcagagccctactag 612

Scoring table: OLIGO.NUC  
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 25

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database : Issued\_Patents\_NA.\*
- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*
  - 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*
  - 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
  - 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
  - 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*
  - 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result      | Query |       |        |    |    |
|-------------|-------|-------|--------|----|----|
| No.         | Score | Match | Length | DB | ID |
| Description |       |       |        |    |    |

No matches found

Search completed: February 22, 2003, 06:08:15  
Job time : 44.5828 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2003, 14:06:16 ; Search time 1849 Seconds  
(without alignments)  
7865.629 Million cell updates/sec

Title: US-09-832-320-1

Perfect score: 898  
Sequence: 1 ctcgcacgcactcgcgcctc.....aaaaaaaaaaaaaaaa 898

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estrov:\*  
6: em\_estrpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vit:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Match | Length | DB | ID       | Description        |
|------------|-------|-------|--------|----|----------|--------------------|
| 1          | 376.6 | 41.9  | 486    | 10 | BE512404 | BE512404 946070F05 |
| 2          | 329.4 | 36.7  | 996    | 12 | BG343299 | BG343299 HVSME000  |
| 3          | 290   | 32.3  | 362    | 13 | BM101325 | BM101325 EBP101.SQ |
| 4          | 207.8 | 23.1  | 681    | 9  | AU082529 | AU082529 AU082529  |
| 5          | 174   | 19.4  | 293    | 9  | AU029886 | AU029886 AU029886  |
| 6          | 142.8 | 15.9  | 500    | 14 | BQ252852 | BQ252852 san81909. |

|    |       |      |     |    |          |                    |
|----|-------|------|-----|----|----------|--------------------|
| 7  | 139   | 15.5 | 759 | 11 | AY106735 | AY106735 Zea mays  |
| 8  | 135.8 | 15.1 | 631 | 13 | BM337818 | BM337818 MEST17-G  |
| 9  | 133.8 | 14.9 | 628 | 12 | BG840355 | BG840355 MEST12-D0 |
| 10 | 133.8 | 14.9 | 663 | 12 | BG873702 | BG873702 MEST9-A05 |
| 11 | 133.8 | 14.9 | 714 | 12 | BG840318 | BG840318 MEST9-A05 |
| 12 | 133.8 | 14.9 | 719 | 13 | BM350281 | BM350281 MEST263-E |
| 13 | 133.8 | 14.9 | 819 | 11 | AY105799 | AY105799 Zea mays  |
| 14 | 132.6 | 14.8 | 539 | 10 | AM678619 | AM678619 WS1_1-B04 |
| 15 | 132.6 | 14.8 | 539 | 10 | BE367566 | BE367566 P11_9-D04 |
| 16 | 132.6 | 14.8 | 568 | 10 | BE367670 | BE367670 P11_9-F05 |
| 17 | 132.6 | 14.8 | 581 | 13 | BM327258 | BM327258 PIC1_11-C |
| 18 | 132.6 | 14.8 | 587 | 13 | BE367638 | BE367638 PIC1_11-C |
| 19 | 132.6 | 14.8 | 587 | 13 | BM330782 | BM330782 PIC1_56-E |
| 20 | 132.6 | 14.8 | 588 | 10 | BE597194 | BE597194 P11_69-C1 |
| 21 | 132.6 | 14.8 | 589 | 10 | BE367530 | BE367530 P11_8-F02 |
| 22 | 132.6 | 14.8 | 593 | 10 | AM678759 | AM678759 WS1_1-B04 |
| 23 | 132.6 | 14.8 | 611 | 10 | BE367671 | BE367671 P11_9-F06 |
| 24 | 132.6 | 14.8 | 634 | 10 | BE600449 | BE600449 P11_9-F06 |
| 25 | 132.6 | 14.8 | 637 | 10 | BE367243 | BE367243 P11_43-D0 |
| 26 | 132.2 | 14.7 | 564 | 12 | BG840588 | BG840588 MEST13-F1 |
| 27 | 132.2 | 14.7 | 611 | 13 | BM072945 | BM072945 MEST56-C0 |
| 28 | 132.2 | 14.7 | 680 | 13 | BM078314 | BM078314 MEST117-H |
| 29 | 131   | 14.6 | 581 | 10 | AM678837 | AM678837 WS1_1-B04 |
| 30 | 131   | 14.6 | 588 | 13 | BM330588 | BM330588 PIC1_53-H |
| 31 | 129.6 | 14.4 | 686 | 13 | BM340658 | BM340658 MEST268-H |
| 32 | 129.4 | 14.4 | 554 | 10 | AM746957 | AM746957 WS1_56-C0 |
| 33 | 126.8 | 14.1 | 616 | 12 | BG842842 | BG842842 MEST40-G0 |
| 34 | 126   | 14.0 | 535 | 13 | BM318608 | BM318608 P11_15-E1 |
| 35 | 122.8 | 13.7 | 595 | 9  | A1861282 | A1861282 603018D05 |
| 36 | 119.8 | 13.3 | 548 | 10 | BE367270 | BE367270 P11_44-E0 |
| 37 | 119.8 | 13.3 | 563 | 13 | BM322997 | BM322997 PIC1_11-C |
| 38 | 119.8 | 13.3 | 564 | 10 | BE367614 | BE367614 P11_9-B10 |
| 39 | 117.2 | 13.1 | 297 | 10 | AM923743 | AM923743 DGL_59-A0 |
| 40 | 117.2 | 13.1 | 550 | 10 | AM671887 | AM671887 LG1_352-H |
| 41 | 116   | 12.9 | 548 | 13 | BM325875 | BM325875 PIC1_53-H |
| 42 | 116   | 12.9 | 575 | 13 | BM326394 | BM326394 PIC1_56-E |
| 43 | 115.6 | 12.9 | 450 | 13 | BT786368 | BT786368 sal36c01  |
| 44 | 114.4 | 12.7 | 438 | 10 | BE601076 | BE601076 P11_96-F0 |
| 45 | 114.4 | 12.7 | 491 | 17 | BH625654 | BH625654 1007108E1 |

## ALIGNMENTS

RESULT 1  
LOCUS BE512404 486 bp mRNA linear EST 07-AUG-2000  
DEFINITION 946070F05.y1 946 - tassal primordialium prepared by Schmidt lab Zea  
ACCESION BE512404  
VERSION BE512404.1 GI:9733652  
KEYWORDS EST.  
SOURCE Zea mays.  
ORGANISM Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Lillipolida; Poales; Poaceae; PRCC  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 486)  
Walbot,V.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Unpublished (1999)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 946070 row: F column: 05.  
Location/Qualifiers  
1..486  
/organism="Zea mays"

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/cultivar="OH43"
/db_xref="taxon:4577"
/clone_lib="946 - tassels primordium prepared by Schmidt
lab"
/tissue_type="tassels"
/dev_stage="just after the transition from vegetative to
inflorescence development"
/lab_host="X10LR"
/notes="Organ: tassels; Vector: HybridAP; Site_1: EcoRI;
Site_2: XhoI; George Chnuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybridAP. Sample insert size range was 350 bp
to 3 kb with a 1 kb average."
BASE COUNT      100 a      131 c      150 g      105 t
ORIGIN
Query Match      41.9%; Score 376.6; DB 10; Length 486;
Best Local Similarity 98.7%; Pred. No. 2.3e-40;
Matches 390; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 469 TGGCGCTGGGTGGCGGAGGGCGGTACTACACCCAGGCAACAGCGCGCGCGG 528
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
47 TGGCGCTGGGTGGCGGAGGGCGGTACTACACCCAGGCAACAGCGCGCGG 105
QY 529 GCGCGAGTGGCGGACGTAACAGCAGTGTGTGGCGCAACACCGCGAGTGGGTGCG 588
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
106 GCGCGAGTGGCGGACGTAACAGCAGTGTGTGGCGCAACACCGCGAGTGGGTGCG 165
QY 589 CCGAGGCGAGTGGCGGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCA 648
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
166 CCGAGGCTTTTGGCGGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCA 225
QY 649 AGGTGAGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 708
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
226 AGGTGAGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 285
QY 709 CAAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 768
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
286 CAAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 345
QY 769 ACGGAAAGCGCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 828
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
346 ACGGAAAGCGCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 405
QY 829 TGGTTGGTGTACAGCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 863
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
406 TGGTTGGTGTACAGCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 440
RESULT 2
BG343299          996 bp  mRNA  linear  EST 22-OCT-2001
LOCUS             BG343299
DEFINITION       HVSMEg0005F16f Hordeum vulgare pre-anthesis spike EST library
HVSMEg0005F16f, mRNA sequence.
ACCESSION        BG343299
VERSION          BG343299.1 GI:13155628
KEYWORDS         EST.
SOURCE           Hordeum vulgare.
ORGANISM         Hordeum vulgare.
REFERENCE        1 (bases 1 to 996)
AUTHORS          Wing, R., Close, T.J., Kleinbols, A., Wise, R., Begum, D., Frisch, D., Yu
, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
, R.D., Close, S.J., Oates, R. and Main, D.
TITLE            Development of a genetically and physically anchored EST resource
for barley genomics: Morex pre-anthesis spike cDNA library
JOURNAL          Unpublished (2001)
COMMENT          Contact: Wing RA
Clemson University Genomics Institute

```

```

100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total bp bases = 471
Seq primer: AATTAACCTCTACTTAAAGG
High quality sequence stop: 717.
Location/Qualifiers
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/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEg0005F16f"
/clone_lib="Hordeum vulgare pre-anthesis spike EST library
HVSMEg0005F16f (white to yellow anther)"
/tissue_type="pre-anthesis spike"
/lab_host="SOLR"
/notes="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
Plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SJ Close, TJ Close). Whole
spike with awns trimmed were collected at white, green and
yellow anther stages (Fenton). Total RNA was prepared from
each pool, equal quantities of all three RNA pools were
combined, poly(A) RNA was purified from the mixture, one
primary unamplified cDNA library was made, and 1 million
plu were in vivo excised to give pluscript SK(-) cDNA
phagmids. These steps were performed in the TJ Close lab
(Choi) at the University of California, Riverside.
Phagmids were plated and picked at the Clemson University
Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins
and Wing) Plasmid DNA preparations, DNA sequencing and
sequence analysis were performed at CUGI (Wing, Yu, Frisch
, Henry, Simmons, Oates, Rambo, Main). The sequence has
been trimmed to remove vector sequence and contains a
minimum of 100 bases of phred value 20 or above. For more
details on library preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders
see Close TJ, Wing R, Kleinbols A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/gnpages/bgn/31/cover.html)"
BASE COUNT      183 a      310 c      377 g      123 t
ORIGIN
Query Match      36.7%; Score 329.4; DB 12; Length 996;
Best Local Similarity 78.3%; Pred. No. 2.1e-34;
Matches 434; Conservative 0; Mismatches 112; Indels 8; Gaps 3;
QY 131 CTTGCGACCCCTCTGCGCTGTGCGCGCGCGCGCGCGCGCGCTCT 190
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
128 CTTCTGCGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 181
QY 191 CATGCGGGGGCGCGCGCGCGGTAACAGGCGGCGGCGGCGGCGGCGGCGG 250
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
182 GCCGCGACGAGAGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 241
QY 251 CAACGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 310
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
242 GAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 301
QY 311 GCGCGCGCTGGGTGAGAACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 370
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
302 GCGCCCGCTGGGTGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 361
QY 371 GCGCGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 430
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
362 GCAAGAAACAGAGAGCTGCGGCTTCCGGGACATGGCGGCGGCGGCGGCGG 421
QY 431 GCGGTGGCGGAGCTACCGCGCGCGCGCGCGGAGGTGTGCGGTGTGCGGAGG 490
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
422 GGGGTGGGCGAGTACCGCGCGCGCGCGGCGGAGGTGTGCGGTCTGCGGTGCG 481

```



|    |     |   |     |
|----|-----|---|-----|
| QY | 491 | GCCATCTACACCCAGCCAAACAACAGCTGGGCGCGGGGGGAGAGTGGCGGACCTACAC      | 550 |
|    |     |   |     |
| Db | 482 | GAAATCTATAGCCCAACGCCCAACAACACTTGGCGCGACGAGAGTGCGCGACCTACAC      | 541 |
| QY | 551 | GCAGTGTGTGTGGCGCAACCGCCGAGAGTGTGGGTGGCGCGCAGGCCAGCTGCCTCACGGG   | 610 |
|    |     |   |     |
| Db | 542 | GCAGGTGTGTGGCGCGCGCCGACCGCGGAGGTGGGTGGGGCGGAGGCCAGCTGGGGCTTCGGG | 601 |
| QY | 611 | GCGCAGCGCTTACGCTTGTGCTTTACACCCGACGGCAGCTGCAGGGGCCAGAGCCCTTA     | 670 |
|    |     |   |     |
| Db | 602 | GCGCAC-CTGACACCTCTTGTCTTTACACCCCG-ACGGGAACGGCGCAGGGCCAGAGACCTTA | 659 |
| QY | 671 | CTAGCTAGCTGAGG  | 684 |
|    |     |   |     |
| Db | 660 | CTAGCCCGACGGGG  | 673 |

| RESULT 3            | LOCUS | DEFINITION                            | ACCESSION | VERSION | KEYWORDS |
|---------------------|-------|---------------------------------------|-----------|---------|----------|
| BM101325            |       |                                       |           |         |          |
| BM101325            |       | 362 bp, mRNA                          |           |         |          |
| EBP101.S0003.I13_R  |       | 11 bp, no treatment, cv Oplic, EBP101 |           |         |          |
| Horidum vulgare     |       | CDNA clone                            |           |         |          |
| EBP101.S0003.I13 5' |       | mRNA sequence.                        |           |         |          |
| BM101325.2          |       | GI:21944137                           |           |         |          |
| EST                 |       |                                       |           |         |          |

ORGANISM  
Hordium vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Angiosperms; Equisetopsida; Magnoliopsida; Liliopsida; Poales; Poaceae; Pooidae;  
Triticeae; Hordium.  
1 (bases 1 to 362)  
REFERENCE  
Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudge, S., Cardle, L.,  
Ramsay, L., Machary, G., Marshall, D.F.M. and Waugh, R.  
TITLE  
Journal of Barley Transcriptome Resources  
COMMENT  
Unpublished (2001)  
On Nov 21, 2001 this sequence version replaced gi:17032393.

Genome Dynamics/Computational Biology  
Scottish Crop Research Institute  
Invergowrie, Dundee, DD2 5DA, Scotland, UK  
Tel: 00 44 1382 562731  
Fax: 00 44 1382 562426  
Email: estescr1.sari.ac.uk  
All sequence has a Phred quality score of 20 or over  
Seq primer: M3 reverse.  
Location/Qualifiers  
1..362  
source

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/dev_stage="1.DPA"
/lab_host="DH09"
/notes="vector: pSPORT1; site_1: Sal I; site_2: Not I;
Non-normalised library, directionally cloned into pSPORT1
derived from 1000 cells dissociated from EBp101"

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|-----------------------|-------|-------------------|----------|
| Best Local Similarity | 32.3% | 290               | 362      |
| Matches               | 87.6% | pred. No. 5,3e-25 |          |
| Conservative          | 0     | Mismatches 45     | Indels 0 |
|                       |       |                   | Gaps 0   |

Db 311 GGGCCCGCTCCGGTGGAGACGGGGGCGTGGCTTCGGCGCGCGCGCGGACCGTGGCGGAGCA 370  
 1 GGGCCCGCTCCGGTGGAGACGGCGCCACCTGACGGCGGGCGGGCGGTGGAGCCCGCTGGAGCA 60

[illegible]

|            |   |
|------------|---|
| RESULT 4   |   |
| AU082529   |   |
| LOCUS      |   |
| DEFINITION | AU082529 681 bp mRNA linear EST 02-APR-2002   |
| ACCESSION  | AU082529 Rice panicle shorter than 3cm Oryza sativa (japonica cultivar-group) cDNA clone E30820, version. |
| VERSION    | AU082529  |
| KEYWORDS   | AU082529.1 GI:6984553   |
| SOURCE     | EST.  |
|            | Oryza sativa (japonica cultivar-group).   |

|           |   |
|-----------|---|
| REFERENCE | Eukaryota; Viridiplantae; Streptophyta; Tracheophyta.   |
| AUTHORS   | Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;   |
| TITLE     | Ehrhartoideae; Oryzaceae; Oryza.  |
| JOURNAL   | 1 (bases 1 to 681)  |
| COMMENT   | Sasaki, T. and Yamamoto, K.<br>Rice cDNA from panicle (2000)<br>Unpublished (2000)<br>Contact: Takuji Sasaki<br>National Institute of Agrobiological Resources<br>Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki |

```

FEATURES
source
location/Qualifiers
1. 681
/organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="F30820"
PROJECT="RGP"
PROJURL="http://rgp.dna.affrc.go.jp/"

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|                       |                                   |                   |                   |
|-----------------------|-----------------------------------|-------------------|-------------------|
|                       | /genome-tip--rice.paricgc.smolder | 1768              | 36m               |
|                       | /dev-stage--shorter               | than 3cm          |                   |
|                       | /note:Organ:                      | panicle           | 141 t             |
| BASE COUNT            | 136 a                             | 187 c             | 214 g             |
| ORIGIN                |                                   |                   | 3 others          |
| Query Match           | 23.1%                             | Score 207.8;      | DB 9; Length 681; |
| Best Local Similarity | 83.5%;                            | Prod No. 1,9e-18; |                   |
| Matches 228;          | Conservative:                     | 0; Mismatches 49; | Indels 2; Gaps 2; |

|           |            |  |            |
|-----------|------------|--|------------|
| <b>QY</b> | <b>424</b> | CAGAACGAGGGGTGGCGAGCTACCGCGCGCGCCGCCGAGGTGTGCGGCTGTGGTGG   | <b>483</b> |
| <b>b</b>  | <b>79</b>  | CGAACCAGGGGT-66CAAGCTACCCGCGCGCGCCCCGCGNAGTGTTGGTCGTGGGTGG | <b>137</b> |

QY 484 CGAGGGGGGCTACTACACCCACACACAGCTGGCGCGGGGGGCGAGTGGGCA 543  
 Db 138 CGAGGGGNNAGTACTACAGCCACACAGCTGGCGCGGGGGGCGAGTGGGCA 197  
 QY 544 CGTACAGCAGAGTGTGTGGGCGCAACACCGCCGAGGTGGGCGCCAGCGCTTGG 603  
 Db 198 CTTACACCCAGGTGTGTGGGCGCGCACGCGAGGTGGGCGCCAGCGCTTGA 257  
 QY 604 CCAAGGGGGCGCGCTGTGTGGGCGCAACCGCCGAGGTGGGCGCGAGTGGGCA 663  
 Db 258 CCAAGGGGGCGCGCTGTGTGGGCGCAACCGCCGAGGTGGGCGCGAGTGGGCA 317  
 QY 664 GCGCCCTACT 672  
 Db 318 GCGCCCTACT 326

## RESULT 5

AU029886  
 LOCUS

DEFINITION AU029886 Rice cDNA from immature leaf including apical meristem  
 Oryza sativa (japonica cultivar-group) cDNA clone E50124\_1A, mRNA

## ACCESSION

AU029886  
 VERSION AU029886.1 GI:3763134

## KEYWORDS

EST.  
 Oryza sativa (japonica cultivar-group).

## SOURCE

Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

## ORGANISM

EST.  
 Oryza sativa (japonica cultivar-group).

## REFERENCE

1 (bases 1 to 293)  
 Sasaki, T. and Yamamoto, K.  
 Rice cDNA from immature leaf including apical meristem  
 Unpublished (1997)  
 Contact: Takuji Sasaki  
 National Institute of Agrobiological Resources  
 Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki  
 305-8602, Japan  
 Tel: 81-298-38-7441  
 Fax: 81-298-38-7468  
 Email: tsasaki@agr.affrc.go.jp, URL: http://rtp.dna.affrc.go.jp/  
 PROJECT = "RGP".  
 POLYA-No.

## AUTHORS

Sasaki, T. and Yamamoto, K.  
 Rice cDNA from immature leaf including apical meristem  
 Unpublished (1997)  
 Contact: Takuji Sasaki  
 National Institute of Agrobiological Resources  
 Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki  
 305-8602, Japan  
 Tel: 81-298-38-7441  
 Fax: 81-298-38-7468  
 Email: tsasaki@agr.affrc.go.jp, URL: http://rtp.dna.affrc.go.jp/  
 PROJECT = "RGP".  
 POLYA-No.

## JOURNAL

Unpublished (1997)  
 Contact: Takuji Sasaki  
 National Institute of Agrobiological Resources  
 Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki  
 305-8602, Japan  
 Tel: 81-298-38-7441  
 Fax: 81-298-38-7468  
 Email: tsasaki@agr.affrc.go.jp, URL: http://rtp.dna.affrc.go.jp/  
 PROJECT = "RGP".  
 POLYA-No.

## COMMENT

Unpublished (1997)  
 Contact: Takuji Sasaki  
 National Institute of Agrobiological Resources  
 Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki  
 305-8602, Japan  
 Tel: 81-298-38-7441  
 Fax: 81-298-38-7468  
 Email: tsasaki@agr.affrc.go.jp, URL: http://rtp.dna.affrc.go.jp/  
 PROJECT = "RGP".  
 POLYA-No.

## FEATURES

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 Location/Qualifiers

## source

1. 293  
 Location/Qualifiers

## FEATURES

1. 293  
 Location/Qualifiers

## source

1. 293  
 Location/Qualifiers

## FEATURES

1. 293  
 Location/Qualifiers

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## FEATURES

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## source

1. 293  
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## FEATURES

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## FEATURES

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 Location/Qualifiers

## source

1. 293  
 Location/Qualifiers

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 QY 560 GTGGCGCAACACCGCGGAGTGGCGCGCGGAGCGAGTGGCGGCGGCGGCGG 619  
 Db 179 GTGGCGCGCGGAGGAGTGGCGGCGGCGGAGCGGAGTGGCGGCGGCGGCGG 237  
 QY 620 CAGCTGTGCTGTGTACACCCGCGGAGCGAGTGGCGGAGCGGCGGCGGCGG 667  
 Db 238 CACATCTGTGTGTACACCCGCGGAGCGGAGTGGCGGAGCGGCGGCGGCGG 284

## RESULT 6

BQ252852  
 LOCUS

DEFINITION BQ252852 500 bp mRNA linear EST 03-MAY-2002  
 san81909.y2 Gm-cl052 Glycine max cDNA clone SOYBEAN CLONE ID:  
 Gm-cl052-6090 5' similar to SW:5714\_S01495 STS14 PROTEIN  
 PRECURSOR. ; mRNA sequence.

## ACCESSION

BQ252852  
 VERSION BQ252852.1 GI:20448728

## KEYWORDS

EST.  
 soybean.

## SOURCE

Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.

## REFERENCE

1 (bases 1 to 500)  
 Shoemaker, R., Kelm, P., Vodkin, L., Epeiding, J., Coryell, V., Khanna  
 A., Bolla, B., Marita, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,  
 Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers  
 Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk  
 R., Rutter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann  
 R., Waterston, R. and Wilson, R.  
 Public Soybean EST Project  
 Unpublished (1999)  
 Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 This clone is available through: Resgen, Invitrogen Corp. 2130  
 South Memorial Parkway Huntsville, AL 35801 For further information  
 call: (800)-533-4363 or contact: ccu@resgen.com web site:  
 www.resgen.com  
 Seq primer: -40RP from gibco  
 High quality sequence stop: 419.

## JOURNAL

Unpublished (1999)  
 Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 This clone is available through: Resgen, Invitrogen Corp. 2130  
 South Memorial Parkway Huntsville, AL 35801 For further information  
 call: (800)-533-4363 or contact: ccu@resgen.com web site:  
 www.resgen.com  
 Seq primer: -40RP from gibco  
 High quality sequence stop: 419.

## COMMENT

Unpublished (1999)  
 Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 This clone is available through: Resgen, Invitrogen Corp. 2130  
 South Memorial Parkway Huntsville, AL 35801 For further information  
 call: (800)-533-4363 or contact: ccu@resgen.com web site:  
 www.resgen.com  
 Seq primer: -40RP from gibco  
 High quality sequence stop: 419.

## FEATURES

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 Location/Qualifiers

## source

1. 500  
 Location/Qualifiers

## FEATURES

1. 500  
 Location/Qualifiers

## source

1. 500  
 Location/Qualifiers

## FEATURES

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 Location/Qualifiers

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 Location/Qualifiers

## FEATURES

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 Location/Qualifiers

## FEATURES

1. 500  
 Location/Qualifiers

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## FEATURES

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1. 500  
 Location/Qualifiers

## FEATURES

1. 500  
 Location/Qualifiers

## source

1. 500  
 Location/Qualifiers

## FEATURES

1. 500  
 Location/Qualifiers

## source

1. 500  
 Location/Qualifiers

## FEATURES

1. 500  
 Location/Qualifiers

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Best Local Similarity 63.1%; Pred. No. 6.6e-10;
Matches 270; Conservative 0; Mismatches 152; Indels 6; Gaps 3;

OY 251 CAACCGGACGCGGACGAGTACCTACCTGCGCGCCGACACACGCGCGCGCGCGCGCGCT 310
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DB 51 CACAGCGCGCGCGGAGGAGTCTTGAGGCGGACACACGAGCAAGAGCCGAAGTGGCGGT 110
    || || || || || || || || || || || || || || || || || || || || || ||
OY 311 GCGCGCGCTGCGGTGGAACGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 370
    || || || || || || || || || || || || || || || || || || || || || ||
DB 111 GGAACCACTTACGTGAGACCGGAGGAGCTGCGAACGTCGATGCTGCTGCTTACCA 170
    || || || || || || || || || || || || || || || || || || || || || ||
OY 371 GCGGCGGAGCGCGGCGCGCTTCCGCGACGTGCGGCGCGCGCGCGCGCGCGCGCGCA 430
    || || || || || || || || || || || || || || || || || || || || || ||
DB 171 GCGGACAAAGAGAGGCTGCGAGTTCGCGGAACTTACGCGCGAGCAAGTACGCGGGA 230
    || || || || || || || || || || || || || || || || || || || || || ||
OY 431 GGGGTGGGC--GAGCTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 487
    || || || || || || || || || || || || || || || || || || || || || ||
DB 231 GCTGCGGCGAGGCGGTGAGCGAGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGTGA 290
    || || || || || || || || || || || || || || || || || || || || || ||
OY 488 GGGGCGGACTACACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 547
    || || || || || || || || || || || || || || || || || || || || || ||
DB 291 GAAGAAATTTACGTCCGCGGAGGAGAACACACGCTGCTGGGGAACACAGAGTCCGCG 350
    || || || || || || || || || || || || || || || || || || || || || ||
OY 358 CACGCACTGCTGTGCGGCAACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 607
    || || || || || || || || || || || || || || || || || || || || || ||
DB 351 TACGCACTGCTGTGAGGAGAACCTGACGAGGTGCGGTGCTCMAAGCCCTGTGTGAA 410
    || || || || || || || || || || || || || || || || || || || || || ||
OY 608 GG--GCGCCACGCTCAACGCTCTGCTGTACACCCCGCGCGCGCGCGCGCGCGAG 664
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DB 411 GGAGAGGCTAGCTTACCATTTTCTTATGACCCACTGCGACGCTATTGGGAGAT 470
    || || || || || || || || || || || || || || || || || || || || || ||
OY 665 CCCCTACT 672
    || || || || || || || || || || || || || || || || || || || || || ||
DB 471 CCCATACT 478
    || || || || || || || || || || || || || || || || || || || || || ||

RESULT 7
A1106735 759 bp mRNA linear HTC 25-MAY-2002
LOCUS Zea mays PC0088779 mRNA sequence.
ACCESSION AY106735
VERSION AY106735.1 GI:21209813
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 759)
REFERENCE Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
AUTHORS Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of
JOURNAL Overgo Probes
REFERENCE Unpublished (2002)
AUTHORS 2 (bases 1 to 759)
TITLE Coe,E.C.
JOURNAL Direct Submission
AUTHORS Submitted (25-APR-2002) Maize Mapping Project, University of
TITLE Missouri, Columbia, MO 65211, USA
FEATURES
SOURCE Location/Qualifiers
1..759
/organism="Zea mays"
/db_xref="MaizeDB:635032"
/db_xref="taxon:4577"
/clone="PC0088779"
/clone_11b="Maize Mapping Project/DuPont Consensus
Library"
/note="this sequence is part of a project of EST
assemblies resulting from the application of public

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BASE COUNT      175 a      229 c      210 g      145 t
ORIGIN
Query Match      15.5%; Score 139; DB 11; Length 759;
Best Local Similarity 61.6%; Pred. No. 1.6e-09;
Matches 258; Conservative 0; Mismatches 155; Indels 6; Gaps 2;

OY 259 CGGCGGACGAGTACTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 318
    || || || || || || || || || || || || || || || || || || || || || ||
DB 152 CGCGGAGACTAGCTGAGCCCGCGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 211
    || || || || || || || || || || || || || || || || || || || || || ||
OY 319 TCGGCTGGAACGCGGCGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 378
    || || || || || || || || || || || || || || || || || || || || || ||
DB 212 TGTCTGTGGAACGACAGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 268
    || || || || || || || || || || || || || || || || || || || || || ||
OY 379 AGGGCGGCTGCGCTTCCGCGGAGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCG 438
    || || || || || || || || || || || || || || || || || || || || || ||
DB 269 GCGACTGCAAGCTGATCCTACCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 328
    || || || || || || || || || || || || || || || || || || || || || ||
OY 439 CGAGTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 498
    || || || || || || || || || || || || || || || || || || || || || ||
DB 329 CGCGCGCGCGACTGTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 388
    || || || || || || || || || || || || || || || || || || || || || ||
OY 499 ACACCCAGCGCGCAACACAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 558
    || || || || || || || || || || || || || || || || || || || || || ||
DB 389 ACAGACACAGCACACACAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 448
    || || || || || || || || || || || || || || || || || || || || || ||
OY 559 TGTGCGGCAACACCGCGGAGGTGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCG 615
    || || || || || || || || || || || || || || || || || || || || || ||
DB 449 TGTGCGGCGACTCCACCGCGCATGCGCTGCGCGCGCGCGCGCGCGCGCGCGCG 508
    || || || || || || || || || || || || || || || || || || || || || ||
OY 616 CGCTACGCTCTGCTGTACACCCCGCGCAACGCTGACGCGCGCGCGCGCGCGCT 674
    || || || || || || || || || || || || || || || || || || || || || ||
DB 509 TCTTCATCATCTGACGATACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 567
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RESULT 8
BM337818/c 631 bp mRNA linear EST 16-JAN-2002
LOCUS BM337818
DEFINITION MEST217-008.T3 ISUM5-RN Zea mays cDNA clone MEST217-G08 3', mRNA
sequence.
ACCESSION BM337818
VERSION BM337818.1 GI:18167978
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 631)
REFERENCE Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S.
AUTHORS Expressed Sequence Tags from B73 Maize: Various Stages and tissues
TITLE Including seedlings treated with a variety of hormones
JOURNAL Unpublished (2001)
AUTHORS Contact: Patrick S. Schnable
COMMENT Schnable Laboratory
Iowa State University
6405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
(http://depts.washington.edu/ventures/collabtr/direct/index.htm*)
rt). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (http://www.tigr.org/softlab/).
Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the

```

poly-T and the high-quality region were replaced with N's to serve as spacers.  
 PCR Primers  
 FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)  
 BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)  
 Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

## FEATURES

Source  
 1. 631  
 /organism="Zea mays"  
 /cultivar="B73"  
 /db\_xref="taxon:4577"  
 /clone="MEST12-D09"  
 /clone\_1lb="ISUM4-TN"  
 /tissue\_type="mixed"  
 /lab\_host="DH10B"  
 /note="Vector: pT73PAC; Site.1: EcoRI; Site.2: NotI; Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG), Mixed mature tissues (17, 21, 38, 69, 77 DAG), Kernels (3, 5, 10, 15, 20, 25, 30, DAG), Adventitious roots (65 DAG), Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0 cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated first ear, ear shank, etiolated seedlings, callus, Cycloheximide-treated callus, Anaerobic treated seedlings, NAA (α-Naphthalene acetic acid)-treated seedlings, Kinetin-treated seedlings, ACPK (1-aminocyclopropane-1-carboxylic acid)-treated seedlings, Brassinolide-treated seedlings, ABA (Abscisic acid)-treated seedlings, GA (Gibberellic acid)-treated seedlings, JA (Jasmonic acid)-treated seedlings. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5', AACTGGAAGAATTTCGGCCGCGAGATTTTCTTTTCTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA Polr-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT73PAC vector. The library then went through one round of normalization to COT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."

## BASE COUNT

123 a 176 c 184 g 148 t

## ORIGIN

Query Match 15.1%; Score 135.8; DB 13; Length 631;  
 Best Local Similarity 61.1%; Pred. No. 4.7e-09;  
 Matches 256; Conservative 0; Mismatches 157; Indels 6; Gaps 2;

259 CGCGGAGAGTACTTGGCGCGCACACACGCGCGCGGCGGTGGCGGTGGCCCGC 318  
 603 CGCGGAGAGTACTTGGCGCGCACACACGCGCGCGCGGTGGCGGTGGCCCGC 544  
 319 TCGGTTGGAACGGCGCGCGCGCGCGCGCGGTGGCGGTGGCCCGC 378  
 543 TGTCTTGGGAGACACCGTCCGCGCGCGGTGGCGGTGGCCCGC 487  
 379 AGGCGGAGTGGCGGTGGCGCGCGCGCGGTGGCGGTGGCCCGC 438  
 486 GCGACTGCGACGCTGATCCTACTCGCGCGCGCGGTGGCGGTGGCCCGC 427  
 439 CGAGTACCGCGCGCGCGCGCGCGGTGGCGGTGGCCCGC 498  
 426 CGCGGCGCGCGGTGGCGCGCGCGGTGGCGGTGGCCCGC 367  
 499 ACACCGACCGCAACACGCTGGCGCGCGCGGTGGCGGTGGCCCGC 558  
 366 ACAGACACGACACACGCTGGCGCGCGGTGGCGGTGGCCCGC 307  
 559 TGTGTTGGAACCGCGCGCGCGCGGTGGCGGTGGCCCGC 615  
 306 TGTGTTGGAACCGCGCGCGCGGTGGCGGTGGCCCGC 247

QY 616 CGCTACGCTGCTGCTGACACCGCGACGCGCGCGGTGGCGGTGGCCCGC 674  
 DB 246 TCTTATCATCTGTCGACGTACACCGCGCGCGGTGGCGGTGGCCCGC 188

RESULT 9  
 BG840355  
 LOCUS  
 DEFINITION  
 sequence.  
 ACCESION  
 BG840355.2 GI:14242662  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Zea mays.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 On May 25, 2001 this sequence version replaced gi:14206677.  
 Contact: Patrick S. Schnable  
 Schnable Laboratory  
 Iowa State University  
 4405 Agronomy, Iowa, State University, Ames, IA 50011-1010, USA  
 Tel: 515-294-0975  
 Fax: 515-294-2299  
 Email: schnable@iastate.edu

PCR Primers  
 FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)  
 BACKWARD: T3 (ATT AAC CCT CAC TAA AG)  
 Seq primer: primer T7-1 (AA TAC GAC TCA CTA TAG).  
 Location/Qualifiers  
 1. 628  
 /organism="Zea mays"  
 /cultivar="B73"  
 /db\_xref="taxon:4577"  
 /clone="MEST12-D09"  
 /clone\_1lb="ISUM4-TN"  
 /tissue\_type="Seedling and silk"  
 /lab\_host="DH10B"  
 /note="Vector: pT73PAC; Site.1: EcoRI; Site.2: NotI; ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5', AACTGGAAGAATTTCGGCCGCGAGATTTTCTTTTCTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA Polr-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT73PAC vector. The library then went through one round of normalization to COT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."

## FEATURES

## source

## BASE COUNT

98 a 210 c 228 g 92 t

## ORIGIN

Query Match 14.9%; Score 133.8; DB 12; Length 628;  
 Best Local Similarity 60.9%; Pred. No. 8.6e-09;  
 Matches 254; Conservative 0; Mismatches 157; Indels 6; Gaps 2;

258 ACAGGAGAGTACTTGGCGCGCACACACGCGCGCGGTGGCGGTGGCCCGC 317  
 106 ACAGGAGAGTACTTGGCGCGCACACACGCGCGCGGTGGCGGTGGCCCGC 165  
 318 CTGCGTTGGAACGGCGCGCGCGGTGGCGGTGGCCCGC 377  
 166 GTGCGTTGGAACGGCGCGCGGTGGCGGTGGCCCGC 225  
 378 CAGGCGGCGGTGGCGCGCGGTGGCGGTGGCCCGC 437

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Db 226 GACTGCGGCTGTGACATCGGGGCGCCGTTGCGGAGAACATC--TTCTGGGGGCTTG 282
QY 438 GCGAGCTACCGCGCGCCGCCGCGAGGTGCTGGGTGGCGAGGGGCGGTAC 497
Db 283 GCGGGGGGGGGCGTGGAGACGGCGCCGACGCGCTCGGTGTGGTACGAGAAGAGAAC 342
QY 498 TACACCCAGCCCAACAACACGTGCGCGGGGCGGAGTGGCGGACGTACAGCAGGTG 557
Db 343 TACACCTGAGCAGACACACTGCGACCCCGCAGCAGTGTGGCGGCACACTACAGCAGGTG 402
QY 558 GTGTGGGCAACACCGCGCGAGTGGGTGGCGCGCAGCCAGCTGGCGC---CACGGGCGCC 614
Db 403 GTGTGGGCGAGGTTCACACCCGATCGGTGCGCGCGCTGTGTGCGCGACACACCGCGGC 462
QY 615 ACGCTCACGCTGTGCTGTACAAACCGCAGCAGCGACAGTGTGCGGCGCAGACCCCTAC 671
Db 463 GTCTTCATGCTGTGACACTACGACCCCGCGGCAACGTCACAGCGCCAGCGCCGTTG 519

```

## RESULT 10

BG873702/c

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LOCUS MEST9-A05.t3 ISUM4-TN Zea mays cDNA clone MEST9-A05 3', mRNA
DEFINITION BG873702 663 bp mRNA linear EST 29-MAY-2001
sequence.
ACCESSION BG873702
VERSION BG873702.1 GI:14245120
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 663)
Olu.F., Cul.F., Guo.L., Ashlock,D.A., Wen,T.J. and Schnable,P.S.
Expressed Sequence tags from B73 Maize Seedlings and Silks
Unpublished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
6405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
PCR Primers
FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
location/Qualifiers
1..663
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone_lib="MEST9-A05"
/clone_1ib="ISUM4-TN"
/tissue_type="Seedling and silk"
/lab_host="DH10B"
/Note="Vector: pT773PAC; Site_1: EcoRI; Site_2: NotI;
ds-cDNA molecules were generated as follows. First-strand
cDNA was prepared from oligo-dT selected mRNA by priming
with a NotI oligo-dT primer (5'
AACTGAGAGATTCGGCGCGCAGAGATTTTCTTTTCTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA Pol. catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pT773PAC vector. The library
then went through one round of normalization to COT value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996)."

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## BASE COUNT

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113 a 218 c 197 g 135 t

```

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Query Match 14.9%; Score 133.8; DB 12; Length 663;
Best Local Similarity 60.9%; Pred. No. 8.3e-09;
Matches 254; Conservative 0; Mismatches 157; Indels 6; Gaps 2;

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QY 258 ACGCGGACAGTACTGTGGCGCGCAACACAGGCGCGCGGTGGCGTGGCGCCG 317
Db 658 ACGCGGACAGTACTGTGGCGCGCAACACAGGCGCGCGGTGGCGTGGCGCCG 599
QY 318 CTGGGCGGAGACCGCGCGCGCTTGGCGCGCGCGCGCGCGCGCGCGCGCG 377
Db 598 GTGGCGGAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 539
QY 378 CAGGCGGCGGTGCGGTTCGCGGACGTGGGGCCAGCCCTTACGGCGCGACAGGGGTGG 437
Db 538 GACTGCGCGGTGTGACATCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 482
QY 438 GCGAGTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 497
Db 481 GCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 422
QY 498 TACACCCAGCCCAACAACACGTGCGCGCGGGGCGCACTGCGGACGTACAGCAGGTG 557
Db 421 TACACCTGAGCAGACACACTGCGACCCCGGCAACGTTGTGGCGCACACGAGGTG 362
QY 558 GTGTGGGCAACACCGCGCGAGTGGGTGGCGCGCAGCCAGCTGGCGC---CACGGGCGCC 614
Db 361 GTGTGGGCGAGGTTCACACCCGATCGGTGCGCGCGCTGTGTGCGCGACACCGCGCG 302
QY 615 ACGCTCACGCTGTGCTGTACAAACCGCAGCAGCGACAGTGTGCGGCGCAGACCCCTAC 671
Db 301 GTCTTCATGCTGTGACACTACGACCCCGCGGCAACGTCACAGCGCCAGCGCCGTTG 245

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## RESULT 11

BG840318

```

LOCUS MEST9-A05.t7-1 ISUM4-TN Zea mays cDNA clone MEST9-A05 5', mRNA
DEFINITION BG840318 714 bp mRNA linear EST 29-MAY-2001
sequence.
ACCESSION BG840318
VERSION BG840318.1 GI:14206640
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 714)
Olu.F., Cul.F., Guo.L., Ashlock,D.A., Wen,T.J. and Schnable,P.S.
Expressed Sequence tags from B73 Maize Seedlings and Silks
Unpublished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
6405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
PCR Primers
FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T7-1 (AA TAC GAC TCA CTA TAG).
location/Qualifiers
1..714
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
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/clone_1ib="ISUM4-TN"
/tissue_type="Seedling and silk"
/lab_host="DH10B"
/Note="Vector: pT773PAC; Site_1: EcoRI; Site_2: NotI;
ds-cDNA molecules were generated as follows. First-strand

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FEATURES
source
1..714
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone_lib="MEST9-A05"
/clone_1ib="ISUM4-TN"
/tissue_type="Seedling and silk"
/lab_host="DH10B"
/Note="Vector: pT773PAC; Site_1: EcoRI; Site_2: NotI;
ds-cDNA molecules were generated as follows. First-strand

```

Individuals, base call and confidence value were assigned using the phred software, <http://depts.washington.edu/ventures/collabtr/direct/index.htm#html>. Overall sequence quality assessment and vector trimming were conducted using the Lucy software (<http://www.ligc.org/soflab/>). PCR parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve as spacers.

PCR Primers  
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)

BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)  
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

```
1. .719
/organism="Zea mays"
/cultivar="B73"
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/clone="MEST263-E11"
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/tissue_type="mixed"
/lab host="DH10B"
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/note="Vector: pT7T3PAC; Site_1: EcoRI; Site_2: NotI;
Tissues: Germinated seed and seed) in as (1, 2, 8, 11 DAG).

```

Mixed mature tissues (1/, 21, 38, 69, 77 DAG), kernels (3, 5, 10, 15, 20, 25, 30, DAG), Adventitious roots (65 DAG)

), Jassiel (3-35 cm, 35 and 50 DAG), immature ear (0.2-3.0 cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated

Cycloheximide-treated callus, Anaerobic treated seedlings

Kinetin-treated seedlings, ACPC

Brassinolide-treated seedlings, ABA (Abscissic acid)-treated seedlings, C<sub>2</sub> (Cibbanelle acid)-treated

seedlings, JA (Jasmonic acid)-treated seedlings. ds-cDNA molecules were generated as follows. First-strand cDNA was

prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5'

resulting DNA:RNA hybrid was treated with RNase H and used

used a template for DNA for catalyzed second strand synthesis. After the addition of *EcoRI* adaptors, the

resulting molecules were directionally cloned into the

then went through one round of normalization to CoT value

Research 6: 791-806, 1996)."

|            |                         |
|------------|-------------------------|
| Similarity | 60.98; Pred. No. 8e-09; |
| Length     | 19;                     |
| DB         | 13;                     |
| Score      | 133.8;                  |
| Length     | 19;                     |
| DB         | 13;                     |
| Score      | 133.8;                  |
| Similarity | 60.98; Pred. No. 8e-09; |

conservative; mismatches 0; indels 0; gaps 2;

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[illegible]

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437

CTGCGCGCTGCTGCACACGCGCGCGCGCGCTTCGCGCGAGAACATC---TTCCTGGGCGCTCG 483

CGAGCTACCGCGCGCGCGCGCGCGCGCGCGAGGTGCTGGCGCTGTGGGTGCGCGAGGGCGGTAC 497

CGGGCGGGCGTGGAGCCGCCGACGCGCTGCCGTCGTGGGTGGACGAGAGAGGAAC 423









|    |     |  |    |
|----|-----|--|----|
| QY | 259 | CGCGGAGACAGTACCTGCGGGCCGCAACACAAAGGGGCGGGGGGGTGGGCCGCCCGC      | 3  |
|    |     |  |    |
| Db | 168 | CGCCGAGAGACTACGTGGACCCGCAACAGCGGGCGGGGCCGACGTGGGGGTGGGGGCTG    | 22 |
| QY | 319 | TGCGGTGAACCGGGGCCCTGGGCTTTCGGCGGCGCGGGGAGGAGCTGGCCACACAGCGGGGC | 37 |
| Db | 228 | TGTCCTGGGAGCAGCAACCGTGGCC---GGGTACGGCGAGAGCTACGGCGGCGAGCGCCAGG | 22 |
| QY | 379 | AGGCGCGGGTGGCCGTTCCGGGACGTGGGGGCCAACCCCTACGGCGCGAACAGAGGGTGG   | 43 |
| Db | 285 | GGGACTGCCAGCTGTATCCACTCCGGCGGGCCCTACGGCGAAGAACCTCTCTGGGGGTCCG  | 34 |
| QY | 439 | CGAGCTACCGGCGCGGCCCGCCGCAAGTGTGTGGCGCTGTGGTGTGGCGGAAGGGCGTACT  | 49 |
| Db | 345 | CGGGCGCCGACTGGTCGGCGCTCCGACGCGCGTGGGCTCTGGGTGTCCGAAACCACTACT   | 40 |
| QY | 499 | ACACCCACCCCAACACAGTGGCGCGCGGGGGCGGACGTGGGCACTACAGCAGAGTGG      | 55 |
| Db | 405 | ACGACCAAGACACCAACAGCTGTCCGGAGAGGGGCAAGTGTGGCCACTTACAGCCAGATGG  | 48 |
| QY | 559 | TGTGGCGCAACCGCGGAGGTGGGGTGGCGGACAGCGCAACTGG---CCACGGGCGCA      | 61 |
| Db | 465 | TGTGGCGCACTCCACCGCCATCGGCTGTGGCCGCTGTCTGGACAAACAGCCCGCG        | 52 |
| QY | 616 | CGCTACAGCTCTGCTGTACAAACCCGACGGAACGTGCAAGGGCCAGGCCCTCTACTAG     | 67 |

[illegible]

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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 806
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (42)..(686)
FEATURE:
NAME/KEY: unsure
LOCATION: (775)
OTHER INFORMATION: The nucleotide at this position may be a o r g t
OTHER INFORMATION: or c.
US-09-257-583-14

Query Match          13.6%; Score 121.8; DB 4; Length 806;
Best Local Similarity 60.6%; Pred. No. 1-Be-13;
Matches 25; Conservative 0; Mismatches 157; Indels 8; Gaps 3,

QY 258 ACGGCGAGCAGTACTGCGCGCCGCAACAACAGCGCCCGCGGCGTGGCGTGGCCCG 317
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 141 ACGCCGAGACTCTCGTAATCTGCACAACCCGCGCGCGGCGAGCGGTGGGCCG 200
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 318 CTGCGGTGAGACCGCGGCCCTCGGTTCGGGCGCGCGGAGAGGTCGACAGCGGCGG 377
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 201 GTGGCGTGGAGCCCAAGGTGGCGCAGTACGCGCAGACTACGCGGCGAAGCGCGCGG 260
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 378 CAGGCGCGGTGCCCGCTGTCGCGAGCTGGGCGGCCACCCCTTACGCGCGGAACCAAGGGTGG 437
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 261 GACTGCGCGGTGGTGCACCTCGGGC---GGCGCGTTCGGCGAGACATCTTCTGGGCTCG 317
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QY 438 GCGAGCTACCGCGCGCGCGCCCGCCGAGGTGGTGGCGCTGTGGGTGGCGAGAGGGCGGTAC 497
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Db 318 GCGGGGCGGGCGCTGGAGCGCGCGCCGCGAGCGGCTGGGTGGGTGGAGAGAGAGAGAAC 377
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QY 498 TACACCCAGCGCAACAACAGCTGCGCGCGGCGGCGAGTGGCGAGTACACACAGGTG 557
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Db 378 TACACCTGAGACAGCAACAGCTGCGAGCCCGGCAAGGTGGCGCACTACAGCAGAGTG 437
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QY 558 GTGTGGCGCA--ACACCGCGAGGTGGGTGGCGCGCAGAGCCAGCTGGCG---CACGGGCG 612
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Db 438 GTGTGGCGCAGGTGTCACCCCGCATCGGTGGCGCGCGGTGCTGTGCTGCCCAACCGCG 497
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QY 613 CCAGCGCTCAGCGTCTGCTGTACACCGCCGACGAGCACTGAGGAGGAGCGCCCTAC 671
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Db 498 GCGTCTTCATGCTGTGAGCTACGACCCCGCGGCACTCAAGCGGCGCGCCCGTTC 556
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RESULT 4
US-08-440-856A-9
Sequence 9, Application US/08440856A
Patent No. 5750873
GENERAL INFORMATION:
APPLICANT: DELAPORTA, STEPHEN L.
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVE. N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,856A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 800

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[illegible]

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1  ?  COUNTRY:  USA
2  ?  ZIP:  61604
3  ?  COMPUTER READABLE FORM:
4  ?  MEDIUM TYPE:  Floppy disk
5  ?  COMPUTER:  IBM PC compatible
6  ?  OPERATING SYSTEM:  PC-DOS/MS-DOS
7  ?  SOFTWARE:  Patentin Release #1.0, Version #1.25
8  ?  CURRENT APPLICATION DATA:
9  ?  APPLICATION NUMBER:  US/07/945, 283
10 ?  FILING DATE:  19920911
11 ?  CLASSIFICATION:  424
12 ?  ATTORNEY/AGENT INFORMATION:
13 ?  NAME:  Ribando, Curtis P
14 ?  REGISTRATION NUMBER:  27976
15 ?  TELECOMMUNICATION INFORMATION:
16 ?  TELEPHONE:  309-685-4011 ext.513
17 ?  TELEFAX:  309-685-4128
18 ?  INFORMATION FOR SEQ ID NO: 1:
19 ?  SEQUENCE CHARACTERISTICS:
20 ?  LENGTH:  8438 base pairs
21 ?  TYPE:  NUCLEIC ACID
22 ?  STRANDEDNESS:  double
23 ?  TOPOLOGY:  linear
24 ?  MOLECULE TYPE:  DNA (genomic)
25 ?  HYPOTHETICAL:  NO
26 ?  ANTI-SENSE:  NO
27 ?  ORIGINAL SOURCE:
28 ?  ORGANISM:  Pseudorabies virus
29 ?  FEATURE:
30 ?  NAME/KEY:  CDS
31 ?  LOCATION:  622..6495
32 ?  FEATURE:
33 ?  NAME/KEY:  variation
34 ?  LOCATION:  replace(1099, "g")
35 ?  FEATURE:
36 ?  NAME/KEY:  variation
37 ?  LOCATION:  replace(1267, "t")
38 ?  FEATURE:
39 ?  NAME/KEY:  variation
40 ?  LOCATION:  replace(1381, "c")
41 ?  FEATURE:
42 ?  NAME/KEY:  variation
43 ?  LOCATION:  replace(1566, "c")
44 ?  FEATURE:
45 ?  NAME/KEY:  variation
46 ?  LOCATION:  replace(7010, "g")
47 ?  US-07-945-283-1
48
49 Query Match 7.8%; Score 70.4; DB 1; Length 8438;
50 Best Local Similarity 49.8%; Pred. No. 0.00022;
51 Matches 262; Conservative 0; Mismatches 256; Indels 8; Gaps 3.
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53 QY 88 ACCTCTCTCTGCTCCCGCGCCCATGAGCCAGCGGCTGCTCTCTGCGACCTCTCTG 147
54 Db 3978 AGCGCGCTTGGCGCGCGGCGGCCCGCGCTCTCTCTGCGCGGCGCGCGTCC 4037
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56 QY 148 GCGTCTGGCGCGCGCGCGCGCGACCCAGCCAGCGCGCGCGTCTCTCATGCGCGCGCGG 207
57 Db 4038 CGCGAGGCGCGCGCGCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGG 4093
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59 QY 208 GCGCGGTACCAAGCGCGAGCGAGGGGTG-GCAACGGAGCGCGCGAGCAACGCGAGCGGAGC 266
60 Db 4094 GCGCGCGCGCGCGCGCGCTTCTTCTTGGCGCGCGTGGGCGGTGGGTCCGGCGCGCGGCG 4153
61
62 QY 267 GAGTACCTGGGCGCGCGCAACCAAGCGCGCGCGCGCGGTGGCGGTGGCGCGCGCGG 326
63 Db 4154 GGGGAGCTGGCGGTACCGCGAGAGAGCGCGGAGCGCGGACTTGTGTCGAGCTGACTTGG 4213
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65 QY 327 AACGCGGCGCTGGCTCTGCGCGCGCGGAGACGCTGGCGGAGACGCGCGAGAGGCGGG 386
66 Db 4214 GTGCTGGAGCGCGGACTTGTCTCTGGCGGCGGTGAGAGGCGCGGAGCGCGGAG 4273
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68 Y 387 TCGCGCTTCGCGGACGTGGGCGCCAGCCCTTACGCGCGGAACCAAGGCGTGGCGGACTTAC 446

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1      APPLICATION NUMBER:  US 07/848,506
2      FILING DATE:  6-MAR-1992
3      PRIOR APPLICATION DATA:
4      APPLICATION NUMBER:  US 07/768,122
5      FILING DATE:  27-SEP-1991
6      PRIOR APPLICATION DATA:
7      APPLICATION NUMBER:  US 07/580,431
8      FILING DATE:  7-SEP-1990
9      PRIOR APPLICATION DATA:
10     APPLICATION NUMBER:  US 07/368,672
11     FILING DATE:  20-JUN-1989
12     PRIOR APPLICATION DATA:
13     APPLICATION NUMBER:  US 07/329,018
14     FILING DATE:  24-MAR-1989
15     PRIOR APPLICATION DATA:
16     APPLICATION NUMBER:  US 08/045,957
17     FILING DATE:  12-APR-1993
18     ATTORNEY/AGENT INFORMATION:
19     NAME:  Elmer James Scott
20     REGISTRATION NUMBER:  36,129
21     REFERENCE/DOCKET NUMBER:  S-19825/P1/GC 1727
22     TELECOMMUNICATION INFORMATION:
23     TELEPHONE:  (919)541-8614
24     TELEFAX:  (919)541-8689
25     INFORMATION FOR SEQ ID NO:  11:
26     SEQUENCE CHARACTERISTICS:
27     LENGTH:  696 base pairs
28     TYPE:  nucleic acid
29     STRANDEDNESS:  single
30     TOPOLOGY:  linear
31     MOLECULE TYPE:  cDNA
32     OS-08-181-271A-11

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INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 696 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-449-315-11

Query Match  
Best Local Similarity 56.2%; Pred. No. 0.0015;  
Matches 122; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

457 CCGCCGAGGTGTGGCTGTGGGTGGCGGCGGCTACTACACCGCAACACA 516  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 319 CCGCTAAGGCGCTGAGATGTGGTCAATGAGAAACAGTATTATGCCACGACTCAACA 378  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 517 CGTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 576  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 379 CTGTGTGCCAAGACAGGTGTGTGGACACTATCTCAGGTGTTGGCTAACTCGGTC 438  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 577 AGGTGGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 636  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 439 GTGTGGATGTGCTAGGGTTCACTGTAACTAGAGATATATTTGCTTGCACACTAG 498  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 637 ACCCGACGCAAGCTGCGAGGCGGCGGCGGCGGCGGCGGCGGCGG 673  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 499 ATCCTCAGGTATGTTATAGGCAAAAGCCCATACTA 535  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

RESULT 9  
US-08-444-803-11  
Sequence 11, Application US/08444803  
Patent No. 5654414  
GENERAL INFORMATION:  
APPLICANT: Ryals, John A.  
APPLICANT: Alexander, Danny C.  
APPLICANT: Beck, James J.  
APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Speerison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericea C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/444,803  
FILING DATE: 19-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271

FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 696 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-444-803-11

Query Match  
Best Local Similarity 56.2%; Pred. No. 0.0015;  
Matches 122; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

457 CCGCCGAGGTGTGGCTGTGGGTGGCGGCGGCGGCTACTACACCGCAACACA 516  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 319 CCGCTAAGGCGCTGAGATGTGGTCAATGAGAAACAGTATTATGCCACGACTCAACA 378  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 517 CGTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 576  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 379 CTGTGTGCCAAGACAGGTGTGTGGACACTATCTCAGGTGTTGGCTAACTCGGTC 438  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
QY 577 AGGTGGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 636  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 439 GTGTGGATGTGCTAGGGTTCACTGTAACTAGAGATATATTTGCTTGCACACTAG 498  
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

QY 637 ACCCGCAGGCACTGCAGGGCCAGAGCCCTACTA 673  
| | | | | | | | | | | | | | | | | | | | | |  
Db 499 ATCTCCAGGTATGTATTAGCAAAAGCCACTACTA 535

## RESULT 10

US-08-449-043-11  
Sequence 11, Application US/08449043  
Patent No. 5689044

## GENERAL INFORMATION:

APPLICANT: Ryals, John A.  
APPLICANT: Alexander, Danny C.  
APPLICANT: Beck, James J.  
APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Melins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericea C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,043  
FILING DATE: 24-MAY-1995  
CLASSIFICATION: 800

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT 1989

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CSC 1727  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689

## INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:  
LENGTH: 696 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-449-043-11

Query Match 7.2%; Score 65; DB 1; Length 696;  
Best Local Similarity 56.2%; Pred. No. 0.0015;  
Matches 122; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 457 CCGCCGAGTGTGGGCGGTGGGTGGCGAGGGCGGTACTACACCCAGCCACACACA 516  
| | | | | | | | | | | | | | | | | | | | | |  
Db 319 CCGCTAAGGCGCGTGAAGTGGGTCAATGAGAAACAGTATTATGCGCCAGCTCAACACA 378  
QY 517 CGTGCAGCGGGGCGCGCAGTGGCGGACGACGAGGTGGTGGCGCAACACCGCGG 576  
| | | | | | | | | | | | | | | | | | | | | |  
Db 379 CTGTGCCAAGACAGAGGTGTGGACACTATACAGTGGTGGTGGCTACTGCGTTTC 438  
QY 577 AGTGGGTTGCGCGCAGCGCAGCTGGCGCCACGCGCGCCACGCTCAAGCTGCTGTACA 636  
| | | | | | | | | | | | | | | | | | | | | |  
Db 439 GTCTTGATGTGCTAGGCTTCACTATACAAATGAGATATATGTTCTTGTCAACTATAG 498

## RESULT 11

US-08-456-265A-11  
Sequence 11, Application US/08456265A  
Patent No. 5767369

## GENERAL INFORMATION:

APPLICANT: Alexander, Danny C.  
APPLICANT: Ryals, John A.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Stinson, Jeffrey R.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 520 White Plains Road, P.O. Box 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: USA

```

ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,265A
FILING DATE: 31-MAY-95
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/181,271
FILING DATE: 13-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 696 base pairs
type: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-456-265A-11
Query Match 7.2%; Score 65; DB 1; Length 696
Best Local Similarity 56.2%; Ptd. No. 0.0015;

```

|   |         |  |              |    |            |     |        |    |      |    |
|---|---------|--|--------------|----|------------|-----|--------|----|------|----|
|   | Matches | 11,  | Conservative | 0; | Mismatches | 95; | Indels | 0; | Gaps | 0; |
| OY  | 457     | CCGCCGAGGTGGTGGCGCTGTGGTGCGCGAGGGGCGGTACTACACCAGCCCAACA    | 516          |    |            |     |        |    |      |    |
| Db  | 319     | CCGGTAAGGCGCCTCGAGATGTGGGTTCATGAAACACGTATTAAAGCCCCAGACTCAA | 378          |    |            |     |        |    |      |    |
| OY  | 517     | CGTGCAGCGGCGGGGCGGACGTGGCGAGCTATACGACGAGTGTGTGGCGCACCGCGG  | 576          |    |            |     |        |    |      |    |
| Db  | 379     | CTTTGGCCCAAGGACACAGGTGTGTGGACACTATACGAGTGTGGTGGCTGAAGTTC   | 438          |    |            |     |        |    |      |    |
| OY  | 577     | AGGTGGGTGCGGCGGACGCGACCTGGCGCCACGCGCCACGCTGACGCTGTGCTGACA  | 636          |    |            |     |        |    |      |    |
| Db  | 439     | GTTGTGATGTGCTAGGAGTTCAETGACAAAGAGGATATATGTCTTTCGACACTANG   | 498          |    |            |     |        |    |      |    |
| OY  | 637     | ACCCGACGCGAACGTGCAGGCGCCAGAGCCCTACTA                       | 673          |    |            |     |        |    |      |    |
| Db  | 499     | ATCCTCCAGGTAAATGTTATAGCCAANAAGCCCATCTA                     | 535          |    |            |     |        |    |      |    |
| <br>RESULT 12<br>US-08-455-416-11<br>; Sequence 11, Application US/08455416<br>; Patent No. 5777200<br>; GENERAL INFORMATION:<br>APPLICANT: Ryals, John A.<br>APPLICANT: Alexander, Danny C.<br>APPLICANT: Beck, James J.<br>APPLICANT: Duesling, John H.<br>APPLICANT: Friedrich, Leslie B.<br>APPLICANT: Goodman, Robert M.<br>APPLICANT: Harms, Christian<br>APPLICANT: Meins, Jr., Frederick<br>APPLICANT: Montoya, Alice<br>APPLICANT: Moyer, Mary B.<br>APPLICANT: Neuhaus, Jean-Marc<br>APPLICANT: Payne, George B.<br>APPLICANT: Sperlison, Christoph<br>APPLICANT: Stinson, Jeffrey R.<br>APPLICANT: Uknes, Scott J.<br>APPLICANT: Williams, Shericea C.<br>TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC<br>NUMBER OF SEQUENCES: 106<br>CORRESPONDENCE ADDRESS:<br>ADDRESSEE: CIBA-GEIGY Corporation<br>STREET: 7 Skyline Drive<br>CITY: Hawthorne<br>STATE: New York<br>COUNTRY: USA<br>ZIP: 10532<br>COMPUTER READABLE FORM:<br>MEDIUM TYPE: Floppy disk<br>OPERATING SYSTEM: IBM PC compatible<br>SOFTWARE: PatentIn Release #1.0, Version #1.25<br>CURRENT APPLICATION DATA:<br>APPLICATION NUMBER: US/08/455,416<br>FILING DATE: 31-MAY-1995<br>CLASSIFICATION: 800<br>PRIOR APPLICATION DATA:<br>APPLICATION NUMBER: 08/181,271<br>FILING DATE: 13-JAN-94<br>APPLICATION NUMBER: US 08/093,301<br>FILING DATE: 16-JUL-1993<br>PRIOR APPLICATION DATA:<br>APPLICATION NUMBER: US 07/937,197<br>FILING DATE: 6-NOV-1992<br>PRIOR APPLICATION DATA:<br>APPLICATION NUMBER: US 07/678,378<br>FILING DATE: 1-APR-1991<br>PRIOR APPLICATION DATA:<br>APPLICATION NUMBER: US 07/305,566 |         |  |              |    |            |     |        |    |      |    |



;; FILING DATE: 6-FEB-1989  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/165,667  
;; FILING DATE: 8-MAR-1988  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/042,847  
;; FILING DATE: 6-APR-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/632,441  
;; FILING DATE: 21-DEC-1990  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/425,504  
;; FILING DATE: 20-OCT-1989  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/848,506  
;; FILING DATE: 6-MAR-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/768,122  
;; FILING DATE: 27-SEP-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/580,431  
;; FILING DATE: 7-SEP-1990  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/368,672  
;; FILING DATE: 20-JUN-1989  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/329,018  
;; FILING DATE: 24-MAR-1989  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/045,957  
;; FILING DATE: 12-APR-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Elmer, James Scott  
;; REGISTRATION NUMBER: 36,129  
;; REFERENCE/DOCKET NUMBER: S-19825/p1/CGC 1727  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (919)541-8614  
;; TELEFAX: (919)541-8689  
;; INFORMATION FOR SEQ ID NO: 11:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 696 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA  
;; US-08-455-416-11

Query Match 7.2%; Score 65; DB 1; Length 696;  
Best Local Similarity 56.2%; Pred. No. 0.0015;  
Matches 122; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

OY 457 CCGCCGAGTGGTGGCGCTGGGTGGCGGAGGGGCGGTACTACACCCAGCCCAACAA 516  
DB 319 CCGCTAAGCCGCTGAGATGGTGGTGCATAGAAACGTTATTTAGCCAGACTCAACA 378  
OY 517 CGTGCCCGCGCGGCGAGTGCAGACGTACAGCAGTGTGTGGCGCAACCGCCG 576  
DB 379 CTGTGCCCGAGACAGAGTGTGTGACACTATCTAGTGTGGCTTGGCGTAATCGGTT 438  
OY 577 AGGTGGGTGGCGCGAGCCAGCTGCGCCACGCGGCGCCACGCTCAGCGCTTGCCTTACA 636  
DB 439 GTGTGGATGTGCTAGAGTTCTAGTGTACATGACATGAGGATATATGTCTTGCACCTANG 498  
OY 637 ACCCGCAGCGCAGTGCAGGCGCAGAGCCCGTACTA 673  
DB 499 ATCTCCAGGTATGTATTAGGCAAAAGCCCATACTA 535

RESULT 13  
US-08-455-244-11  
; Sequence 11, Application US/08455244  
; Patent No. 5789214  
; GENERAL INFORMATION:

;; APPLICANT: Ryals, John A.  
;; APPLICANT: Alexander, Danny C.  
;; APPLICANT: Beck, James J.  
;; APPLICANT: Duesing, John H.  
;; APPLICANT: Friedrich, Leslie B.  
;; APPLICANT: Goodman, Robert M.  
;; APPLICANT: Harms, Christian  
;; APPLICANT: Meins, Jr., Frederick  
;; APPLICANT: Montoya, Alice  
;; APPLICANT: Moyer, Mary B.  
;; APPLICANT: Neuhaus, Jean-Marc  
;; APPLICANT: Payne, George B.  
;; APPLICANT: Sperison, Christoph  
;; APPLICANT: Stinson, Jeffrey R.  
;; APPLICANT: Uknes, Scott J.  
;; APPLICANT: Ward, Eric R.  
;; APPLICANT: Williams, Sheriecca C.  
;; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
;; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
;; NUMBER OF SEQUENCES: 106  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: CIBA-GEIGY Corporation  
;; STREET: 7 Skyline Drive  
;; CITY: Hawthorne  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 10532

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,244  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672



```
Best Local Similarity 56.2%; Pred. No. 0.0015;
Matches 122; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 457 CCGCGAGGTGGTGGCCGTGGTGGCGGAGGGCGGTACTACACCGCAACACA 516
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 319 CCGCTAAGCGCGTGAATGGTGCATATGAGAAACAGTATTGTGCCAGACTCAAA 378
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 517 CGTGCGCCGCGGCGGCGAGTGGCGGACGTACACGAGTGTGTGGCGCAACCGCG 576
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 379 CTTGTGCCAAGGACAGGTGTGTGACACTATCTACAGGTGGTGGCTTAACCTCGGTT 438
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 577 AGTGGGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 636
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 439 GTGTGATGTGTAGGTTGATGTATACATGAGGATATTTCTTTCGACTATG 498
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 637 ACCGCGACGCGACGTGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 673
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 499 ATCCTCCAGGTATGTATAGGCMAAGCCCATACTA 535
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
US-08-457-364-11
; Sequence 11, Application US/08457364
; Patent No. 5847258
; GENERAL INFORMATION:
; APPLICANT: Rivals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhans, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericea C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,364
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 696 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-457-364-11

Query Match 7.2%; Score 65; DB 2; Length 696;
Best Local Similarity 56.2%; Pred. No. 0.0015;
Matches 122; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 457 CCGCGAGGTGGTGGCCGTGGTGGCGGAGGGCGGTACTACACCGCAACACA 516
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 319 CCGCTAAGCGCGTGCAGATGTGGGTCAATGAGAAACAGTATTGTGCCAGACTCAAA 378
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 517 CGTGCGCCGCGGCGGCGAGTGGCGGACGTACACGAGTGTGTGGCGCAACCGCG 576
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 379 CTTGTGCCAAGGACAGGTGTGTGACACTATCTACAGGTGGTGGCTTAACCTCGGTT 438
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 577 AGTGGGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 636
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 439 GTGTGATGTGTAGGTTGATGTATACATGAGGATATTTCTTTCGACTATG 498
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 637 ACCGCGACGCGACGTGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 673
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 499 ATCCTCCAGGTATGTATAGGCMAAGCCCATACTA 535
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Search completed: March 18, 2003, 15:03:06
Job time : 143 secs
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[illegible]

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RESULT 2
US-09-832-320-3
: Sequence 3, Application US/09832320
: Patent No. US20010049834A1
: GENERAL INFORMATION:
: APPLICANT: Crane, Edmund H.
: APPLICANT: Crane, Virginia C.
: TITLE OF INVENTION: Male Pathogenesis-Related
: TITLE OF INVENTION: Polynucleotide and Methods of Use
: FILE REFERENCE: 35718/214291
: CURRENT APPLICATION NUMBER: US/09/832,320
: CURRENT FILING DATE: 2001-04-10
: PRIOR APPLICATION NUMBER: US 60/195,801
: PRIOR FILING DATE: 2000-04-10
: NUMBER OF SEQ ID NOS: 3
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 612
: TYPE: DNA
: ORGANISM: Zea mays
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(612)
US-09-832-320-3

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|                       |                 |                     |           |             |
|-----------------------|-----------------|---------------------|-----------|-------------|
| Query Match           | 68.2%;          | Score 612;          | DB 10;    | Length 612; |
| Best Local Similarity | 100.0%;         | Pred. No. 3.7e-101; |           |             |
| Matches 612;          | Conservative 0; | Mismatches 0;       | Indels 0; | Gaps 0;     |

|    |     |   |     |
|----|-----|---|-----|
| QY | 63  | ATGAGCGACTGCGGAGCGACACACACATCTCTCTCTCCGCGGCGCCATATGCGACAGGCG      | 122 |
| Db | 1   | ATGAGCGACTGCGGAGCGACACACACATCTCTCTCTCCGCGGCGCCATATGCGACAGGCG      | 60  |
| QY | 123 | TGCTGTGCTCTGCGACACCCCTCTCTGCGGCTTGCGGCGCGCGCGCGCGCGACCGACGGCGCG   | 182 |
| Db | 61  | TGCTGTGCTCTGCGACACCCCTCTCTGCGGCTTGCGGCGCGCGCGCGCGCGACCGACGGCGCG   | 120 |
| QY | 183 | CGCGTCCCTATGCGCGGCGCGCGCGCGCGCGCGCGCTGACCAAGCGCAGCAGGCTGGACACGCG  | 242 |
| Db | 121 | CGCGTCCCTATGCGCGGCGCGCGCGCGCGCGCGCTGACCAAGCGCAGCAGGCTGGACACGCG    | 180 |
| QY | 243 | AGCGCGACGACACCGGACGCGGCGGAGAGTACTGTGGCGCGGACACCAAGGCGCGCGCGCG     | 302 |
| Db | 181 | AGCGCGACGACACCGGACGCGGCGGAGAGTACTGTGGCGCGGACACCAAGGCGCGCGCGCG     | 240 |
| QY | 303 | GTGGGCGTGGCCCCCGCTGCGGTTGGGAACCGCGGCGCTTGCGTGGCGCGCGCGGCGGACGTTG  | 362 |
| Db | 241 | GTGGGCGTGGCCCCCGCTGCGGTTGGGAACCGCGGCGCTTGCGTGGCGCGCGCGGCGGACGTTG  | 300 |
| QY | 363 | GCGGAGGAGGGGCGGCGGAGGGCGGGGTGGCGCTTGCGGCGAGCTGGGGGCGACCCCTACGCG   | 422 |
| Db | 301 | GCGGAGGAGGGGCGGCGGAGGGCGGGGTGGCGCTTGCGGCGAGCTGGGGGCGACCCCTACGCG   | 360 |
| QY | 423 | GCGAACCAGGGGTGGGCGAGCTACCGCGCGCGCGCGCGCGAGGTGGTGGCGCTGTGGGTG      | 482 |
| Db | 361 | GCGAACCAGGGGTGGGCGAGCTACCGCGCGCGCGCGCGCGAGGTGGTGGCGCTGTGGGTG      | 420 |
| QY | 483 | GCGAGGAGGGCGGTACTACACCGACGCCAACAACAGTGGCGCCCGCGGGCGCGCATGCGCG     | 542 |
| Db | 421 | GCGAGGAGGGCGGTACTACACCGACGCCAACAACAGTGGCGCCCGCGGGCGCGCATGCGCG     | 480 |
| QY | 543 | ACGTACACGCAAGTGTGTGTGGCGCAACACCGCGGAGGTGGGGTGGCGGCGAGCGCACTGTG    | 602 |
| Db | 481 | ACGTACACGCAAGTGTGTGTGGCGCAACACCGCGGAGGTGGGGTGGCGGCGAGCGCACTGTG    | 540 |
| QY | 603 | GCCACGCGGCGCGCATGCTACACCTTGCTGTACAAACCGACGCGACGCGCAACGTGCAGGGCCAG | 662 |
| Db | 541 | GCCACGCGGCGCGCATGCTACACCTTGCTGTACAAACCGACGCGCAACGTGCAGGGCGCAG     | 600 |
| QY | 663 | AGCCCTACTAG 674   |     |
| Db | 601 | AGCCCTACTAG 612   |     |

```

RESULT 3
US-09-840-479-12
: Sequence 12, Application US/09840479
: Patent No. US20010025380A1
: GENERAL INFORMATION:
: APPLICANT: Crane, Virginia
: TITLE OF INVENTION: Family Of Maize PR-1 Genes And Promoters
: FILE REFERENCE: 5718-32, 035718/175219
: CURRENT APPLICATION NUMBER: US/09/840, 479
: CURRENT FILING DATE: 2001-04-23
: PRIOR APPLICATION NUMBER: 09/257, 583
: PRIOR FILING DATE: 1999-02-25
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 12
: LENGTH: 749
: TYPE: DNA
: ORGANISM: Zea mays
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (92)..(583)
US-09-840-479-12

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Db 126 ACGCCGACGAGCTGCTGTAATCTGCACAAACCGCGCGCGCGGCGGAGCGCTGGGCCG 185  
QY 318 CTGCGGTGAAGCGGGGCTTGCTGGCGCGCGCGGAGCGTGGCCAGAGCGGGG 377  
Db 186 GTGGCTGGGAGCGGAGGCTGAGTACAGAGCTACGCGGAGGCGCGCGG 245  
QY 378 CAGGCGGGTGGCGCTTCCGACGAGTGGGGCCAGCCCTACGCGGAGAACCGAGGTGG 437  
Db 246 GACTGGCGGCTGTGACCTCGGGC---GGCGGTTGGGAGAGATCTTCTGGGGCTCG 302  
QY 438 GCGAGCTACCGCGCGCGCGCGCGCGAGTGTGGCGCTGTGGTGGCGGAGCGGCTAC 497  
Db 303 GCGGGCGGGCGCTGTGAGCGCGCGCGAGCGCTGCGGTCTGGTGGAGAGAGGAGAAC 362  
QY 498 TACACCGACGCAACAGACGAGTGGCGCGGGGCGGAGTGGGCGAGCTACGAGAGG 557  
Db 363 TACACCTGAGCAGCAGACACTGCGACCGCGGAGAGTGTGGCGACTACAGCGAGG 422  
QY 558 GTGTGGCGCA--ACACCGCGGAGTGGCGGCGCGAGGCGAGCTGCGC--CACGGGCG 612  
Db 423 GTGTGGCGGAGGTGCTCCACCGCGAGTGGCGCGCGCTGCTGGCGCGAGAACCGG 482  
QY 613 CCAGCTCAGCGCTGCTGCTGTACACCGCGAGCGAGCTGACGAGGCGGAGCGCTAC 671  
Db 483 GCGTCTTCACTGCTGCTGAGCTACGACCGCGCGGAGAGCTCAACGAGCGCGCGCTTC 541

RESULT 6  
US-09-840-479-14  
Sequence 14, Application US/09840479  
Patent No. US20010025380A1  
GENERAL INFORMATION:

APPLICANT: Crane, Virginia  
TITLE OF INVENTION: Family of Maize PR-1 Genes And Promoters  
FILE REFERENCE: 5718-32, 035718/175219  
CURRENT APPLICATION NUMBER: US/09/840,479  
CURRENT FILING DATE: 2001-04-23  
PRIOR APPLICATION NUMBER: 09/257,583  
PRIOR FILING DATE: 1999-02-25  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 14  
LENGTH: 806  
TYPE: DNA  
ORGANISM: zea mays  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (42)..(686)  
NAME/KEY: unsure  
LOCATION: (775)  
OTHER INFORMATION: The nucleotide at this position may be a or g or t  
US-09-840-479-14

Query Match 13.6%; Score 121.8; DB 10; Length 806;  
Best Local Similarity 60.6%; Pred. No. 1.6e-13;  
Matches 254; Conservative 0; Mismatches 157; Indels 8; Gaps 3;

QY 258 ACGGCGGACGAGTACTGCGGCGCGCAGCAACAGGCGCGCGCGGTGGCGGCGCCG 317  
Db 141 ACCCGGAGAGACTTCTGATTCGACAAACCGCGCGCGCGCGCGCGCGCGCGCG 200  
QY 318 CTGCGGTGAAGCGGGGCTGGCTTGGCGCGCGCGCGGAGCGAGTGGCGAGCGCGG 377  
Db 201 GTGGCGGTGAGACCGCAGGTGGCGAGGTACGCGAGCTACGCGCGGAGCGCGCGG 260  
QY 378 CAGGCGGAGTGGCGCTTGGCGGAGCGTGGGGCGAGCCCTTACGCGCGGAGAGGGGTG 437  
Db 261 GACTGGCGGCTGTGACTCGGGC---GGCGCTGGCGGAGAGCATCTTCTGGGGCTCG 317  
QY 438 GCGAGCTACCGCGCGCGCGCGCGCGAGTGTGGCGCTGTGGTGGCGGAGGCGCGTAC 497  
Db 318 GCGGGCGGGCGGTGAGCGCGCGCGCGCGCGCGTGTGGTGGAGAGAGAGAGAAC 377

QY 498 TACACCGACGCAACAGACGTCGCGCGCGCGGAGTGGCGAGCTACAGCGAGTGG 557  
Db 378 TACACCTGAGCAGCAGACACTGTGGACCGCGGAGAGTGTGGCGCACTACAGCGAGTGG 437  
QY 558 GTGTGGCGCA--ACACCGCGGAGTGGGTGGCGCGCAGCGCTGCTGCGC---CACGGGCG 612  
Db 438 GTGTGGCGGAGGTGTCCACCGCGAGTGGCGCTGCGCGCGCGCTGCTGCGCGAGAACCGG 497  
QY 613 CCAGCTCAGCGCTGCTGCTGTACAAACCGCGAGGCAACGTCGAGGCGAGGCGCGCTAC 671  
Db 498 GCGTCTTCACTGCTGCTGAGCTACGACCGCGCGGAGAGCTCAACGCGCGCGCGCTTC 556

RESULT 7  
US-10-068-347-3  
Sequence 3, Application US/10068347  
Patent No. US20020166146A1  
GENERAL INFORMATION:

APPLICANT: Pioneer Hi-Bred International, Inc.  
APPLICANT: Simmons, Carl  
APPLICANT: Acevedo, Pedro  
APPLICANT: Crane, Virginia  
TITLE OF INVENTION: Maize PRL Polynucleotides and Methods of Use  
FILE REFERENCE: 35718/242798 (5718-151)  
CURRENT APPLICATION NUMBER: US/10/068,347  
CURRENT FILING DATE: 2002-02-06  
PRIOR APPLICATION NUMBER: 60/267,052  
PRIOR FILING DATE: 2001-02-07  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Patentln version 3.0  
SEQ ID NO 3  
LENGTH: 772  
TYPE: DNA  
ORGANISM: zea mays  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (56)..(571)  
US-10-068-347-3

Query Match 13.2%; Score 118.8; DB 9; Length 772;  
Best Local Similarity 59.7%; Pred. No. 5.4e-13;  
Matches 258; Conservative 0; Mismatches 162; Indels 12; Gaps 3;

QY 258 ACGGCGGACGAGTACTGCGCGCGCAGCAACAGGCGCGCGCGGTGGCGGCGCCG 317  
Db 149 ACGGCGGAGACTTCTGTAATCTGACACACTCCCGCGCGCGGAGCGTGGCGGAGAAC 208  
QY 318 CTGCGGTGAAGCGGGGCTTGGCTTGGCGCGCGCGGAGCGAGTGGCGAGCGCGCG 377  
Db 209 GTGGCTGTGAACACACAGGTGG---CGCGCTACCGCGAGCTACGCGAGAACACCGCGCG 265  
QY 378 CAGGCGGAGTGGCGGCTTGGCGGAGGTGGGGCGAGCCCTTACAGGCGGAGAGGGTGG 437  
Db 266 GCGGACTGCGGCTGTGCTCACTCCGCGGCGCTACGCGGAGAACCTGTTCTGGGCTCG 325  
QY 438 GCGAGCTACCGCGCGCGCGCGCGAGGTGGTGGCTGTGGTGGCGGAGAGGGCGGTAC 497  
Db 326 GCGGCTACGCTGTGAGCGCGCTGCAACGCGCTGGGATCTCGCGCGCGGAGAGAGACTAC 385  
QY 318 CTGCGGTGAAGCGGGGCTTGGCTTGGCGCGCGCGGAGCGAGTGGCGAGCGCGCG 377  
Db 209 GTGGCTGTGAACACACAGGTGG---CGCGCTACCGCGAGCTACGCGAGAACACCGCGCG 265  
QY 378 CAGGCGGAGTGGCGGCTTGGCGGAGGTGGGGCGAGCCCTTACAGGCGGAGAGGGTGG 437  
Db 266 GCGGACTGCGGCTGTGCTCACTCCGCGGCGCTACGCGGAGAACCTGTTCTGGGCTCG 325  
QY 438 GCGAGCTACCGCGCGCGCGCGCGAGGTGGTGGCTGTGGTGGCGGAGAGGGCGGTAC 497  
Db 326 GCGGCTACGCTGTGAGCGCGCTGCAACGCGCTGGGATCTCGCGCGCGGAGAGAGACTAC 385  
QY 498 TACACCGACGCAACAGACGTCGCGCG---CGGGCGGCGAGTGGCGGCGAGCTACAG 551  
Db 386 TACAACCGACGCGACCAACACCTGCTCGCTCCGCTCGCGAGTGTGTTGCTACCTAC 445  
QY 552 CAGGTGTGTGGCGGAAACAGCGCGAGGTGGGTGGCGGC---AGGCGAGTGGCGGACG 608  
Db 446 CAGTGTGTGGCGCGCGCTTCCACTGCTGATGCGGAGTGGCGCGCGCGCTGCTGAGAAC 505  
QY 609 GCGGCGAGCTCAGCTGCTGCTGTACAAACCGCGAGGCAACGTCGAGGCGGAGCGCC 668  
Db 506 GCGGCGCTTCACTGATCATGTGCAACATATTACCGCGGCAACGTCGATTGGACAGAGCCCT 565  
QY 669 TACTAGCTAGCT 680





| QY | 379 | AGGGGGGGTGGCGCTTCGGGACGCTGGGGGAGCCACCCCTACGGGGGACACCGAGGGGTGGG     | 4338 |
|----|-----|--|------|
|    | Db  | 202 ACTGCACTGTGTGATTCCTGGGCGGGCAGTACGGGAGAGAACATTTACGGAGAGCCGGCGG  | 261  |
| QY | 439 | CGAGCTACCGCGCGCGCCCGCCGACAGGTGTGTGGCTGTGGGTGGCGAGAGGGGGGTACT       | 498  |
|    | Db  | 262 GCGGGGCGGACTGGAGCCGCCCGGACGCCGTGTGCACAGGTGGTGTGTGCGAGAGGAGTACT | 321  |
| QY | 499 | ACACCACCGCCACACACGAGTGGCGCGCGGGGGGGGCA-----GTGGGGCACGTACACGC       | 552  |
|    | Db  | 322 ACGACACAGCGGACGACACAGCTGCTCGGCGCGCGGACACAGTCTGCTTGCACACTACACGC | 381  |
| QY | 553 | AGGTGTGTGGCGGACACCGCGCAGGTGGGTGGCGCGCAGGCGAGTGGCGCCACCGG--         | 610  |
|    | Db  | 382 AGGTGTGTGGCGGACGACTCGACGGCCATCGGCTGCGCGCGGTGTGTGTGGACGCGCGCG   | 441  |
| QY | 611 | -CGGCACGCTACGCTGCTGCTTACACACCGGACCGGACAAAGTACGAGGGCGACGGCCCT       | 669  |
|    | Db  | 442 ACGGCGTGTTCATCATCTGCGAGCTACAAACCGCGGGGCACTACGAGAGGGGTGAGCCAT   | 501  |
| QY | 670 | ACTAG 674  |      |
|    | Db  | 502 ACTAG 506  |      |

```

RESULT 10
US-10-068-347-9
Sequence 9, Application US/10068347
Patent No. US20020166146A1
GENERAL INFORMATION:
APPLICANT: Pioneer Hi-Bred International, Inc.
APPLICANT: Simmons, Carl
APPLICANT: Acevedo, Pedro
APPLICANT: Crane, Virginia
TITLE OF INVENTION: Maize P1 Polynucleotides and Methods of Use
FILE REFERENCE: 35718/242798 (5718-151)
CURRENT APPLICATION NUMBER: US/10/068,347
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: 60/2267,052
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 525
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(285)
US-10-068-347-9

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|                           |        |                    |           |             |
|---------------------------|--------|--------------------|-----------|-------------|
| Query Match               | 12.0%; | Score 107.6;       | DB 9;     | Length 525; |
| Best Local Similarity     | 62.0%; | Pred. No. 5.1e-11; |           |             |
| Matches 170; Conservative | 0;     | Mismatches 104;    | Indels 0; | Gaps 0;     |

[illegible]

Db 282 CTAAGCTAGCTTAGCACTCAGTACCCTCGG 315

```

RESULT 11
US-10-078-929-97
; Sequence 97, Application US/10078929
; Patent No. US20020152497A1
; GENERAL INFORMATION:

```

APPLICANT: Rafalski, Antoni  
 APPLICANT: Miao, Guo-Hua  
 APPLICANT: Falco, Saverio Carl  
 APPLICANT: Sakai, Hajime  
 APPLICANT: Remodu, Omolayo O.  
 APPLICANT: Ogelli, Joan T.  
 APPLICANT: Meyers, Blake  
 APPLICANT: Thorpe, Catherine  
 APPLICANT: Weng, Zude

```

CURRENT APPLICATION NUMBER: US/10/078,929
CURRENT FILING DATE: 2002-02-19
PRIORITY APPLICATION NUMBER: 09/566,394
PRIORITY FILING DATE: 2000-05-05
PRIORITY APPLICATION NUMBER: 60/133038
PRIORITY FILING DATE: 1999-05-07
PRIORITY APPLICATION NUMBER: 60/133042
PRIORITY FILING DATE: 1999-05-07
PRIORITY APPLICATION NUMBER: 60/133427
PRIORITY FILING DATE: 1999-05-11
PRIORITY APPLICATION NUMBER: 60/133437
PRIORITY FILING DATE: 1999-05-11
PRIORITY APPLICATION NUMBER: 60/133428
PRIORITY FILING DATE: 1999-05-11
PRIORITY APPLICATION NUMBER: 60/133438
PRIORITY FILING DATE: 1999-05-11
PRIORITY APPLICATION NUMBER: 60/133436
PRIORITY FILING DATE: 1999-05-11
PRIORITY APPLICATION NUMBER: 60/137667
PRIORITY FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 208
SOFTWARE: Microsoft Office 97
SEQ ID NO 97

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|---|------------------|---------------------|--|
| ? | 1125.3           | DATA                |  |
| ? | ORGANISM:        | Trillicium aestivum |  |
| ? | FEATURE:         |                     |  |
| ? | NAME/KEY:        | unsure              |  |
| ? | LOCATION:        | (44.5)              |  |
| ? | NAME/KEY:        | unsure              |  |
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| ? | NAME/KEY:        | unsure              |  |
| ? | LOCATION:        | (51.8)              |  |
| ? | NAME/KEY:        | unsure              |  |
| ? | LOCATION:        | (53.4)              |  |
| ? | NAME/KEY:        | unsure              |  |
| ? | LOCATION:        | (55.8)              |  |
| ? | NAME/KEY:        | unsure              |  |
| ? | LOCATION:        | (54.7)              |  |
| ? | DS-10-078-929-97 |                     |  |

|                       |              |                    |                 |             |
|-----------------------|--------------|--------------------|-----------------|-------------|
| Query Match           | 10.98;       | Score 98;          | DB 12;          | Length 547; |
| Best Local Similarity | 55.98;       | Pred. No. 2.6e-09; |                 |             |
| Matches 228;          | Conservative | 0;                 | Mismatches 172; | Indels 8;   |
|                       |              |                    |                 | Gaps 2;     |

|    |     |  |     |
|----|-----|--|-----|
| QY | 259 | CCGCGACAGTACCTGGCGCGCGACAAACCGGCGCGCGGGGCGGTGGGCGGTGGCGCCCGC | 318 |
| Db | 82  | CGCCGAGACTTCTGTGACCCCGACACCGCGCGCGCGCGCGACGTCCGCTTCGGCGCCG   | 141 |
| QY | 319 | TGGGTGGAACCGGGCCCTGGCTTCGGCGGCGCGGGGACGGTGGCGGACGACGCGGCGCGC | 378 |
| Db | 142 | TGACCTGGGACCAACTGTGGCCCATACGCGAGAACTACCGGAGAGCGCGCGCGC       | 201 |



|                       |        |                    |       |             |
|-----------------------|--------|--------------------|-------|-------------|
| Query Match           | 8.0%;  | Score 72.2;        | DB 9; | Length 492; |
| Best Local Similarity | 50.6%; | Pred. No. 0.00011; |       |             |

[illegible]





GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

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Run on:      March 18, 2003, 10:55:25 ; Search time 272 Seconds
              (without alignments)
              7434.906 Million cell updates/sec
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Title: US-09-832-320-1
Perfect score: 898
Sequence: 1 ctgcgcgcactcgaagctc.....aaaaaaaaaaaaaaaa 898
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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|                  |               |              |
|------------------|---------------|--------------|
| Post-processing: | Minimum Match | 0%           |
|                  | Maximum Match | 100%         |
|                  | Listing first | 45 summaries |

Database : N\_Geneseq\_101002:\*

|     |  |
|-----|--|
| 1:  | /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*  |
| 2:  | /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*  |
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| 8:  | /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*  |
| 9:  | /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*  |
| 10: | /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*  |
| 11: | /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*  |
| 12: | /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*  |
| 13: | /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*  |
| 14: | /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*  |
| 15: | /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*  |
| 16: | /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*  |
| 17: | /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*  |
| 18: | /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*  |
| 19: | /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*  |
| 20: | /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*  |
| 21: | /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*  |
| 22: | /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:* |
| 23: | /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:* |
| 24: | /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*  |

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID       | Description        |
|------------|-------|-------------|--------|----|----------|--------------------|
| 1          | 898   | 100.0       | 898    | 24 | ABA96417 | Maize PRL-C10 codo |
| 2          | 612   | 68.2        | 612    | 24 | ABA96418 | Maize PRL-C10 codo |
| 3          | 140.6 | 15.7        | 731    | 16 | AAQ95804 | PR-1 like gene PR  |
| 4          | 139   | 15.5        | 749    | 20 | AAZ21207 | Zea mays pathogene |
| 5          | 137.6 | 15.3        | 866    | 20 | AAZ21191 | Zea mays pathogene |
| 6          | 121.8 | 13.6        | 806    | 20 | AAZ21194 | Zea mays pathogene |
| 7          | 105   | 11.7        | 846    | 24 | ABL50008 | Nucleotide sequenc |
| 8          | 85.2  | 9.5         | 679    | 21 | AAC43084 | Arabidopsis thalia |
| 9          | 83.6  | 9.3         | 683    | 21 | AAC37078 | Arabidopsis thalia |

|   |    |      |     |        |    |          |                      |
|---|----|------|-----|--------|----|----------|----------------------|
| C | 10 | 83.4 | 9.3 | 114955 | 20 | AAY53491 | Human adenosine A    |
|   | 11 | 81.6 | 9.1 | 114955 | 20 | AAX53491 | Human adenosine A    |
|   | 12 | 72.2 | 8.0 | 779    | 21 | AAC47173 | Arabidopsis thaliana |
|   | 13 | 71.2 | 7.9 | 664    | 24 | ABL59002 | Nucleotide sequence  |
|   | 14 | 70.4 | 7.8 | 8438   | 15 | ABQ73500 | DNA encoding Pseud   |
|   | 15 | 70   | 7.8 | 712    | 24 | ABO40858 | Oligonucleotide f    |
| C | 16 | 70   | 7.8 | 712    | 24 | ABO40859 | Oligonucleotide f    |
| C | 17 | 69.8 | 7.8 | 65140  | 22 | ADH17184 | Streptomyces nours   |
| C | 18 | 69.8 | 7.8 | 125401 | 22 | AAH17186 | Streptomyces nours   |
| C | 19 | 69.6 | 7.8 | 3198   | 20 | AAQ2974  | Human IL-1ra BAC C   |
|   | 20 | 69   | 7.7 | 1983   | 22 | ABA54513 | Fucan exohydrolai    |
|   | 21 | 68   | 7.6 | 679    | 24 | ABF59001 | Nucleotide sequenc   |
| C | 22 | 67.8 | 7.6 | 12561  | 22 | AAH26500 | Rabbit low density   |
| C | 23 | 67.6 | 7.5 | 117213 | 19 | AAH62176 | HSV-2 strain S95 C   |
| C | 24 | 67.6 | 7.5 | 154746 | 24 | AAD25519 | Human herpesvirus    |
| C | 25 | 66.4 | 7.4 | 881    | 24 | ABQ29954 | Oligonucleotide fo   |
|   | 26 | 66.4 | 7.4 | 881    | 24 | ABQ29955 | Oligonucleotide fo   |
|   | 27 | 66.2 | 7.4 | 1281   | 13 | AAQ23296 | HSV-1 (NGH-10) IC    |
|   | 28 | 66.2 | 7.4 | 2561   | 22 | AAH26500 | Rabbit low density   |
| C | 29 | 66   | 7.3 | 27541  | 22 | AAH17185 | Streptomyces nours   |
| C | 30 | 65.8 | 7.3 | 25360  | 22 | AAF88314 | S. spinoza DNA fra   |
| C | 31 | 65.8 | 7.3 | 29736  | 22 | AAF88317 | S. spinoza DNA fra   |
|   | 32 | 65.2 | 7.3 | 3957   | 22 | AAA09686 | HSV-2 immediate ea   |
|   | 33 | 65.2 | 7.3 | 154746 | 24 | AAD25519 | Human herpesvirsu    |
|   | 34 | 65   | 7.2 | 696    | 11 | AAQ06182 | PR-1c cDNA cloned    |
|   | 35 | 65   | 7.2 | 696    | 20 | AAV62807 | Tobacco PR-1c gene   |
|   | 36 | 65   | 7.2 | 696    | 20 | AAV72899 | PR-1c protein enco   |
|   | 37 | 65   | 7.2 | 721    | 10 | AAH91021 | Nicotiana tabacum    |
| C | 38 | 65   | 7.2 | 24379  | 18 | AAH91021 | Streptomyces freno   |
| C | 39 | 65   | 7.2 | 24379  | 19 | AAV25925 | Streptomyces roseo   |
|   | 40 | 65   | 7.2 | 27541  | 22 | AAH17185 | Streptomyces nours   |
|   | 41 | 65   | 7.2 | 125401 | 22 | AAH17186 | Streptomyces nours   |
|   | 42 | 64.6 | 7.2 | 4653   | 22 | AAF30931 | Maize p-glycoprote   |
|   | 43 | 64.6 | 7.2 | 8036   | 22 | AAH30930 | Maize p-glycoprote   |
| C | 44 | 64.4 | 7.2 | 4257   | 19 | AAV68520 | The nucleotide seq   |
| C | 45 | 64.4 | 7.2 | 4257   | 19 | AAV10362 | Infected cell prot   |

## ALIGNMENTS

|          |   |
|----------|---|
| RESULT 1 |   |
| ABA96417 |   |
| ID       | ABA96417 standard; CDNA; 898 BP.                              |
| XX       |   |
| AC       | ABA96417;   |
| XX       |   |
| DT       | 02-APR-2002 (first entry)                                     |
| XX       |   |
| DE       | Maize PRL-C10 encoding CDNA SEQ ID NO 1.                      |
| XX       |   |
| KW       | Maize; pathogen-related; PRL-C10; plant; transgenic; gene; ss |
| XX       |   |
| OS       | Zea mays.   |
| XX       |   |
| Key      | Location/Qualifiers   |
| FH       | 63..674   |
| CDS      | /*tag= a  |
| FT       | /product= "PRL-C10"   |
| XX       |   |
| EN       | US2001049834-A1.  |
| XX       |   |
| PD       | 06-DEC-2001.  |
| XX       |   |
| PF       | 10-APR-2001; 2001US-0832320.                                  |
| XX       |   |
| PR       | 10-APR-2000; 2000US-195801P.                                  |
| XX       |   |
| PA       | ((CRAN/)) CRANE E H.  |
| XX       |   |
| PI       | ((CRAN/)) CRANE V C.  |
| XX       |   |
| XX       | Crane EH, Crane VC;   |





QY 303 GTGGGGTGGCCCCGCTGCGGTGGAAACGCGGGCTTGGGCGGCGCGGGGAGCGGTG 362  
 |||||  
 Db 241 GTGGGGTGGCCCCGCTGCGGTGGAAACGCGGGCTTGGGCGGCGCGGGGAGCGGTG 300  
 |||||  
 QY 363 GCGCAGCAGCGCGCGGAGGCGGGGTGCGGCTTGGCGGAGCTGGGGGCGAGCCCTACGCGC 422  
 |||||  
 Db 301 GCGCAGCAGCGCGGAGGCGGGGTGCGGCTTGGCGGAGCTGGGGGCGAGCCCTACGCGC 360  
 |||||  
 QY 423 GCGAACCGAGGGGTGGGAGAGTACCGCGGGCGCGCGGAGCTGGTGGCGCTGGGGGTG 482  
 |||||  
 Db 361 GCGAACCGAGGGGTGGGAGAGTACCGCGGGCGCGCGGAGCTGGTGGCGCTGGGGGTG 420  
 |||||  
 QY 483 GCGGAGGGGCGGTACTACACCCACGCGCAACACAGCTGGCGGCGGGGAGAGTGGCGC 542  
 |||||  
 Db 421 GCGGAGGGGCGGTACTACACCCACGCGCAACACAGCTGGCGGCGGGGAGAGTGGCGC 480  
 |||||  
 QY 543 ACGTACACCGAGGTGGTGGGCGCAACACCGCGGAGGTGGTGGCGGAGCGCAGCTGC 602  
 |||||  
 Db 481 ACGTACACCGAGGTGGTGGGCGCAACACCGCGGAGGTGGTGGCGGAGCGCAGCTGC 540  
 |||||  
 QY 603 GCCACGCGCGCAGCTACGCTGCTGTACAAACCGGCAAGCGGAGCTGCGAGGCGCAG 662  
 |||||  
 Db 541 GCCACGCGCGCAGCTACGCTGCTGTACAAACCGGCAAGCGGAGCTGCGAGGCGCAG 600  
 |||||  
 QY 663 AGCCCTACTAG 674  
 |||||  
 Db 601 AGCCCTACTAG 612

## RESULT 3

AAQ99804  
 ID AAQ99804 standard; cDNA; 731 BP.

AC AAQ99804;

DT 20-JUN-1996 (first entry)

DE PR-1 like gene PR-1mz.

XX SAR; tobacco; protein-synthesis independent gene; cyclohexamide;  
 KM systemic acquired resistance response; anti-pathogen; plant protection;  
 KW maize; PR-1; ss.

OS Zea mays.

XX Key Location/Qualifiers  
 FH CDS 40..531  
 FT /\*\*tag- a

PN W09519443-A2.

XX 20-JUL-1995.

PD 03-JAN-1995; 95WO-IB00002.

PR 13-JAN-1994; 94US-0181271.

XX (CIBA ) CIBA GEIGY AG.

XX Alexander DC, Ryals JA, Uknes SJ, Ward ER;

DR WPI; 1995-263872/34.

XX P-PSDB; AAR91595.

XX New DNA cont. plant systemic acquired resistance genes - and  
 PT transgenic plants cont. them, impart disease and pest resistance,  
 PR also Arabidopsis gene promoter to control DNA transcription

PS Claim 21; Page 70; 85pp; English.

XX This sequence represents the DNA sequence of a maize PR-1 like gene,  
 CC PR-1mz. This sequence was isolated by screening a BTH-induced cDNA

CC Library of maize. The library was screened using a probe matching to  
 CC the PR-1 barley clone HVR1BR. This sequence, AAQ99800-Q99803 and  
 CC AAQ99805 are all used in recombinant/chimeric DNA molecules of the  
 CC invention. These sequences were isolated by differential screening of a  
 CC cDNA library, followed by analysis by Northern hybridisation to RNA in  
 CC the presence and absence of cyclohexamide. The genes are used in the  
 CC creation of transgenic plants. All of these sequences confer  
 CC anti-pathogenic properties to transgenic plants. Transgenic expression  
 CC of 2 or more of the recombinant molecules of the invention that encode  
 CC anti-pathogenic proteins provides a synergistic increase in plant  
 CC protection, and may also offer protection against a wider range of  
 CC pathogens.  
 XX

SQ Sequence 731 BP; 186 A; 212 C; 199 G; 134 T; 0 other;

Query Match 15.7%; Score 140.6; DB 16; Length 731;  
 Best Local Similarity 61.8%; Pred. No. 1.1e-12;  
 Matches 259; Conservative 0; Mismatches 154; Indels 6; Gaps 2;

QY 259 CGGGGAGAGTACCTGCGCGCGGACCAACAGCGCGCGGCGGTGGCGCCCGC 318  
 |||||  
 Db 116 CGCGGAGAGTACCTGCGCGCGGACCAACAGCGCGCGGCGGTGGCGCCCGC 175  
 |||||  
 QY 319 TGCGTGGAACGCGCGGCGCTGCTGCGCGCGGCGGAGCGGTGGCGCGCGC 378  
 |||||  
 Db 176 TGTCTTGGAGAGACCGGTGGCC---GCTACGCGGAGAGCTACGCGCGCAGCGCAGG 232  
 |||||  
 QY 379 AGGGCGGCGCGGCTTGGCGGAGGTGGGCGCAGCCCTACGCGCGGAGCGGTGGG 438  
 |||||  
 Db 233 GCGACTGCAAGCTGATCCTCCTCGGCGGCGCTTACGCGGAGAACCTCTTGGGGCTCGG 292  
 |||||  
 QY 439 CGAGCTACCGCGCGCGCGCGCGGAGGTGGTGGCGCTTGGGTGGCGGAGGCGGTACT 498  
 |||||  
 Db 293 CCGGCGCGGAGTGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 352  
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 QY 499 ACAACCGCAGCAACACAGCTGCGCGCGCGGCGGAGGTGGCGCGCGCGCGCGCGCG 558  
 |||||  
 Db 353 ACGACGACGACACACACAGCTGCGCGGAGGAGGAGGTGGCGCGCGCGCGCGCGCGCG 412  
 |||||  
 QY 559 TGTGGCGCAACCGCGCGGAGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 615  
 |||||  
 Db 413 TGTGGCGCGAGCTCCACCGCATCGCTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 472  
 |||||  
 QY 616 CGGTCAGCGCTGCTGCTGTACAAACCGGCAAGCTGCGCGCGCGCGCGCGCGCGCG 674  
 |||||  
 Db 473 TCTTCATCATCTGACCTACACCGCGCGGCAAGCTGCTGCGCGAGAGCCCTACTAG 531  
 |||||

## RESULT 4

AAZ21207  
 ID AAZ21207 standard; DNA; 749 BP.

AC AAZ21207;

DT 22-NOV-1999 (first entry)

DE Zea mays pathogenesis-related class I PR-1#83 gene.

XX Zea mays; maize; pathogenesis-related class I; PR-1; promoter;  
 KW regulation; expression; disease resistance; genetic manipulation;  
 KW tobacco mosaic virus; cucumber mosaic virus; ringspot virus;  
 KW necrosis virus; maize dwarf virus; viroid; bacterial; insect;  
 KW nematode; fungal; ss.

OS Zea mays.

XX Key Location/Qualifiers  
 FH CDS 92..583  
 FT /\*\*tag= a  
 FT /product= "PR-1#83"  
 FT /note= "pathogenesis-related class I protein"

PN W09943819-A1.

```

XX 02-SEP-1999.
PD
XX 11-FEB-1999; 99WO-US03011.
PF
XX 26-FEB-1998; 98US-0076100.
PR
XX 27-MAR-1998; 98US-0079648.
PA
XX (PION-) PIONEER HI-BRED INT INC.
PI
XX Crane VC;
XX
XX WPI; 1999-527621/44.
DR
XX P-PSDB; AA129944.
XX
XX New promoter sequences from pathogenesis-related genes of maize -
XX
XX Example 3; Page 72-73; 86pp; English.
XX
XX AA22186 to AA22190 represents the nucleotide sequences for promoters
XX isolated from a family of maize (Zea mays) genes encoding pathogenesis
XX related (PR-1) proteins. The promoters are useful for expressing
XX heterologous genes (including genes for disease resistance) in plants,
XX especially dicots, or monocots i.e. maize. The promoters are useful for
XX the genetic manipulation of plants to exhibit specific phenotypes,
XX particularly enhanced resistance to pathogen-caused disease. Pathogens
XX include viruses such as tobacco or cucumber mosaic virus, ringspot
XX virus, necrosis virus, and maize dwarf virus, and viroids, bacteria,
XX insects, nematodes and fungi. The present sequence encodes a maize
XX PR-1 protein given in the present invention.
XX
XX Sequence 749 BP; 160 A; 235 C; 206 G; 148 T; 0 other;

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Query Match 15.5%; Score 139; DB 20; Length 749;
Best Local Similarity 61.6%; Pred. No. 1.8e-12;
Matches 258; Conservative 0; Mismatches 135; Indels 6; Gaps 2;

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OY 259 CGCGGAGCAGTACTGTGGCGCCGACACACAGCGCGCGGTGGCGTGGCCCGC 318
DB 168 CGCGGAGCAGTACTGTGGCGCCGACACACAGCGCGCGGTGGCGTGGCCCGC 227
OY 319 TGGGTGGAGACGGGGGCTTGGCGCGCGCGCGCGCGGTGGCGTGGCCCGC 378
DB 228 TGTCTGGAGGACGACCGGTGGCGCGCGCGCGCGGTGGCGTGGCCCGC 284
OY 379 AGGCGGAGTGGCGGTGGCGCGCGCGCGCGCGGTGGCGTGGCCCGC 438
DB 285 GGCAGTGGCAGTGGCGGTGGCGCGCGCGCGCGGTGGCGTGGCCCGC 344
OY 439 CGAGTACCGCGCGCGCGCGCGCGCGCGGTGGCGTGGCCCGC 498
DB 345 CGCGGAGCAGTACTGTGGCGCCGACACACAGCGCGCGGTGGCGTGGCCCGC 404
OY 499 ACACCGCAGCAGTGGCGCGCGCGCGCGGTGGCGTGGCCCGC 558
DB 405 ACACCGCAGCAGTGGCGCGCGCGCGCGGTGGCGTGGCCCGC 464
OY 559 TGTGGGCAACACCGCGCGCGCGCGGTGGCGTGGCCCGC 615
DB 465 TGTGGGCAACACCGCGCGCGCGCGGTGGCGTGGCCCGC 524
OY 616 CGGTACCGTGGCGGTGGCGCGCGCGGTGGCGTGGCCCGC 674
DB 525 TCTTCATCATCTGACGTACACACCGCGCGCGGTGGCGTGGCCCGC 583

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```

RESULT 5
AA221191
ID AA221191 standard; DNA; 866 BP.
XX
AC AA221191;
XX
DT 22-NOV-1999 (first entry)

```

```

XX Zea mays pathogenesis-related class I PR-1#52 gene.
DE
XX Zea mays; maize; pathogenesis-related class I; PR-1; promoter;
KW regulation; expression; disease resistance; genetic manipulation;
KW tobacco mosaic virus; cucumber mosaic virus; ringspot virus;
KW necrosis virus; maize dwarf virus; viroid; bacterial; insect;
KW nematode; fungal; ss.
XX
XX Zea mays.
OS
XX
XX Key Location/Qualifiers
FH 111..581
FT CDS /*tag= a
FT /*product= "PR-1#52"
FT /*note= "pathogenesis-related class I protein"

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```

WO9943819-A1.
XX
XX 02-SEP-1999.
PD
XX 11-FEB-1999; 99WO-US03011.
PF
XX 26-FEB-1998; 98US-0076100.
PR
XX 27-MAR-1998; 98US-0079648.
PA
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Crane VC;
XX
XX WPI; 1999-527621/44.
DR
XX P-PSDB; AA129940.
XX
XX New promoter sequences from pathogenesis-related genes of maize -
XX
XX Claim 22; Page 65-66; 86pp; English.
XX
XX AA22186 to AA22190 represents the nucleotide sequences for promoters
XX isolated from a family of maize (Zea mays) genes encoding pathogenesis
XX related (PR-1) proteins. The promoters are useful for expressing
XX heterologous genes (including genes for disease resistance) in plants,
XX especially dicots, or monocots i.e. maize. The promoters are useful for
XX the genetic manipulation of plants to exhibit specific phenotypes,
XX particularly enhanced resistance to pathogen-caused disease. Pathogens
XX include viruses such as tobacco or cucumber mosaic virus, ringspot
XX virus, necrosis virus, and maize dwarf virus, and viroids, bacteria,
XX insects, nematodes and fungi. The present sequence encodes a maize
XX PR-1 protein given in the present invention.
XX
XX Sequence 866 BP; 213 A; 228 C; 240 G; 185 T; 0 other;

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Query Match 15.3%; Score 137.6; DB 20; Length 866;
Best Local Similarity 62.4%; Pred. No. 3e-12;
Matches 267; Conservative 0; Mismatches 154; Indels 7; Gaps 3;

```

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OY 259 CGCGGAGCAGTACTGTGGCGCCGACACACAGCGCGCGGTGGCGTGGCCCGC 318
DB 145 CGCGGAGCAGTACTGTGGCGCCGACACACAGCGCGCGGTGGCGTGGCCCGC 204
OY 319 TGGGTGGAGACGGGGGCTTGGCGCGCGCGCGCGGTGGCGTGGCCCGC 378
DB 205 TGTCTGGAGTGAACAGTGGCGCGCGCGCGGTGGCGTGGCCCGC 264
OY 379 AGGCGGAGTGGCGGTGGCGCGCGCGCGGTGGCGTGGCCCGC 438
DB 265 ACTGCACACTGTGGTGGCGCGCGCGCGCGGTGGCGTGGCCCGC 324
OY 439 CGAGTACCGCGCGCGCGCGCGCGCGGTGGCGTGGCCCGC 495
DB 325 GCGGCGGCGCGCGCGCGCGCGCGGTGGCGTGGCCCGC 384
OY 496 ACTACACCGCAGCAGCAGTGGCGCGCGCGCGGTGGCGTGGCCCGC 555

```

DB 385 ACTAGATTACAAACGCAACAGCTGCGGCGGGAGGTGTGCGGCACCTACACGCAAG 444  
 QY 556 TGGTGTGGCGCAACACCGCGAGTGGGTGGCGGAGCCAGCTGGCGCACGGGC---G 612  
 DB 445 TGTGTGGGCAAA-ATCCCCGCGCATCGGCTGGCCCGGCTGTGTGCAACACAGCGGTG 503  
 QY 613 CCAGCTCAGCGCTGTGCTGTACAAACCGCACGAGGTGAGGGCCAGAGCCCTACT 672  
 DB 504 GCGTCTTCATCAGCTGCAACTACACCGCGCGCACTCCGCGAGACAGACCTACT 563  
 QY 672 AGCTAGCT 680  
 DB 564 AGCTAGCT 571

## RESULT 6

AAZ21194  
 ID AAZ21194 standard; DNA; 806 BP.

AC AAZ21194;

DT 22-NOV-1999 (first entry)

DE Zea mays pathogenesis-related class I PR-1#93 gene.

KM Zea mays; maize; pathogenesis-related class I; PR-1; promoter;  
 KM regulation; expression; disease resistance; genetic manipulation;  
 KM tobacco mosaic virus; cucumber mosaic virus; ringspot virus;  
 KM necrosis virus; maize dwarf virus; viroid; bacterial; insect;  
 KM nematode; fungal; ss.

OS Zea mays.

XX Key Location/Qualifiers  
 FH 42..686  
 FT CDS

FT /tag= a  
 FT /product= "PR-1#93"  
 FT /note= "pathogenesis-related class I protein"

PN W09943819-A1.

PD 02-SEP-1999.

XX 11-FEB-1999; 99WO-US03011.

XX 26-FEB-1998; 98US-0076100.

XX 27-MAR-1998; 98US-0079648.

PA (PRON-) PIONEER HI-BRED INT INC.

XX Crane VC;

DR WPI; 1999-527621/44.

XX P-PSDB; AAY29943.

XX New promoter sequences from pathogenesis-related genes of maize

PS Claim 22; Page 74-75; 86pp; English.

XX AAZ21186 to AAZ21190 represents the nucleotide sequences for promoters  
 CC isolated from a family of maize (Zea mays) genes encoding pathogenesis  
 CC related (PR-1) proteins. The promoters are useful for expressing  
 CC heterologous genes (including genes for disease resistance) in plants,  
 CC especially dicots, or monocots i.e. maize. The promoters are useful for  
 CC the genetic manipulation of plants to exhibit specific phenotypes,  
 CC particularly enhanced resistance to pathogen-caused disease. Pathogens  
 CC include viruses such as tobacco or cucumber mosaic virus, ringspot  
 CC virus, necrosis virus, and maize dwarf virus, and viroids, bacteria,  
 CC insects, nematodes and fungi. The present sequence encodes a maize  
 CC PR-1 protein given in the present invention.  
 SQ Sequence 806 BP; 158 A; 243 C; 260 G; 144 T; 1 other;

Query Match 13.6%; Score 121.8; DB 20; Length 806;  
 Best Local Similarity 60.6%; Pred. No. 6.6e-10;  
 Matches 254; Conservative 0; Mismatches 157; Indels 8; Gaps 3;

QY 258 ACGCGGAGCAGATACCTGAGCGCCGACACMACAGCGCGCGGTGGGCGGCGGCGG 317  
 DB 141 ACGCGGAGGAGCTTCGTGAATCTGCACAAACCGCGCGCGCGCGGAGCGCGGTGG 200  
 QY 318 CTGGGTGTGAACGCGGCGCTTGCTTGCGCGCGCGCGGAGCGGTGACGACGCGCG 377  
 DB 201 GTGGCGTGGGAGACGACGAGGTGGCGAGGTACGCGGAGCTACGCGGCGGCGG 260  
 QY 378 CAGGCGGAGTGGCGGTTCGCGGAGCGGTGGCGGCGGCGGCGGCGGCGGCGGCGG 437  
 DB 261 GACTGCCGCGCTGTGTGCACTGGGC---GGCGCTTGGCGGAGCAATCTTGTGGGCTG 317  
 QY 438 GCGAGTACCGCGCGCGCCCGCGAGGTGGTGGCGCTGTGGGCGGAGGCGGCTAC 497  
 DB 318 GCGGCGCGGCGCGTGGAGCGCGCGGAGCGCGCTCGGTCGTGGTGTGACGAGAGAG 377  
 QY 498 TACACCGACCGCAACACACAGTGCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 557  
 DB 378 TACCACCTGAGCAGCAACACCTGCGACCCGCGCAAGGTGTGGCGCCTACACGAGGTG 437  
 QY 558 GTGTGGGCA--ACACCGCGAGTGGGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 612  
 DB 438 GTGTGGGCGAGGTGTGTCCACCGCATGGCTGGCGGCGGCGGTCTGCGCGGACACGCG 497  
 QY 613 CCAGCTCAGCGCTGCTGCTGTACAAACCGCACGCGCAACGTGACGAGCGGCGGCTAC 671  
 DB 498 GCGTCTTCATCGTCTGAGCTACGACCCCGGCGCAACGTCAACGCGCACGCGCGCTTC 556

## RESULT 7

ABL59008  
 ID ABL59008 standard; DNA; 846 BP.

AC ABL59008;

DT 20-AUG-2002 (first entry)

DE Nucleotide sequence of an antibacterial protein.

XX Antibacterial protein; microbe resistance; plant; gene; ss.

XX Elaeis guineensis.

OS Key Location/Qualifiers  
 FH 35..523  
 FT CDS

FT /tag= a  
 FT /product= "antibacterial protein"

PN JP2002095477-A.

PD 02-APR-2002.

XX 20-SEP-2000; 2000JP-0285905.

XX 20-SEP-2000; 2000JP-0285905.

PA (MITU) MITSUBISHI CHEM CORP.

PA (BADA-) BADAN PENGKAJIAN DAN PENERAPAN TEKNOLOGI.

PA (PAR-) PT PAKRIE BROS.

PA (BIOI-) BIOINDUSTRI KYOKAI SH.

PA (DOKU-) DOKURITSU GIOSEI HOJIN SANGYO GIJUTSU SO.

DR WPI; 2002-439987/47.

XX P-PSDB; ABB77767.  
 XX New protein and its gene, useful for creating plants with high  
 XX resistance to pathogenic microbes -  
 PS Claim 3; Page 8-9; 13pp; Japanese.

XX The present sequence encodes a polypeptide which has antibacterial  
CC activity. The antibacterial protein and its polynucleotide can be used  
CC for the creation of a plant with resistance against pathogenic microbes  
XX  
XX Sequence 846 BP; 218 A; 208 C; 214 G; 206 T; 0 other;

|                           |        |                    |            |             |
|---------------------------|--------|--------------------|------------|-------------|
| Query Match               | 11.7%; | Score 105;         | DB 24;     | Length 846; |
| Best Local Similarity     | 56.1%; | Pred. No. 2.1e-07; |            |             |
| Matches 245; Conservative | 0;     | Mismatches 180;    | Indels 12; | Gaps 2;     |

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| Oy       | 265  | AACAGTACTGGCGCCGCAACAACACAGCGCGCGCGGGCGGTGGCGCTGCCGCGCGCGT       | 328 |
| Db       | 120  | AAACACTTTGTGAGCGCCCAACAACGACGCCGGCGCGCTGTGGCGCTGCCTGGGTGCT       | 179 |
| Oy       | 325  | GGAACCGCGGCTTGCGCTTCGCGCGCGCGCGGAGCGGTGCGCAGCACGCGCGCAGGGCG      | 384 |
| Db       | 180  | GGGACAAACACCGTGGCAGCGCTTAACGCCAAGAATACGCAACACAGCGGAAATCGCGCATCGC | 239 |
| Oy       | 385  | GGTGGCGGTTCCGGGACGTGGGGGCGAACCCCTTAGCGCGCGCAACCAAGGGGTGGCGAGCT   | 444 |
| Db       | 240  | AGCTTCGTCCACTCCGGCGC-----GACCCTACGGGTGAAGACCTCTTCTGGGGATCAG      | 290 |
| Oy       | 445  | ACCGCGCGGGCGCCC---GCCGAGGTGGTGGCGGTGGTGGCGGAGGGGCGGTACTACA       | 501 |
| Db       | 291  | GTAGGGGATACACCGCAGCGGTGCTGTGAACCTTGTGGGTAGTGAAGACAGTGTACG        | 350 |
| Oy       | 502  | CCCCAGCCAACAACAGTGGCGCGCGGGGCGGCAGTGCAGCACAGCAGCAGCGAGTGTGT      | 561 |
| Db       | 351  | ACTACAGACAAACAACTTGCGCGCGCGGGAAAGTGTGCGGTCACTACCAACCGAGTGGTGT    | 410 |
| Oy       | 562  | GGCGCAACACCCGCCGAGGTGCGGTGCGCGCAGCGCACTGCGCCACGGCGCCACGCTCA      | 621 |
| Db       | 411  | GGCGAGACTCCACCCACATCGGCTGCGCTCGGGTGAATCAACAATGGCGCACTTTA         | 470 |
| Oy       | 622  | CGGCTGCCCTGTACACCCCGCAGCGCAACGTGCAGGGCGACCCCTACTAGTACGTG         | 681 |
| Db       | 471  | TTCATTGCAACACTACCAACTCCGGGCAATATGCTGGGGCGAGCGCCATTTAGTATAG       | 530 |
| Oy       | 682  | AGGTCAATCAGGTGCTAG   | 698 |
| Db       | 531  | CCGGGCTCTTCATCG  | 547 |
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| AAC49084 |  |  |     |
| ID       | AAC49084 standard; DNA; 679 BP.                                |  |     |
| XX       | AAC49084;  |  |     |
| AC       |  |  |     |
| XX       |  |  |     |
| DT       | 18-OCT-2000 (first entry)                                      |  |     |
| XX       |  |  |     |
| DE       | Arabidopsis thaliana DNA fragment SEQ ID NO: 59865.            |  |     |
| XX       |  |  |     |
| KW       | Hybridisation assay; genetic mapping; gene expression control; |  |     |
| KM       | protein identification; signal transduction pathway;           |  |     |
| XX       | metabolic pathway; promoter; termination sequence; ss.         |  |     |
| OS       | Arabidopsis thaliana.  |  |     |
| PN       | EPI033405-AZ.  |  |     |
| XX       |  |  |     |
| PD       | 06-SEP-2000.   |  |     |
| PP       |  |  |     |
| XX       | 25-FEB-2000; 2000EP-0301439.                                   |  |     |
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| PR       | 05-MAR-1999; 990S-0123180.                                     |  |     |
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DE Arabidopsis thaliana DNA fragment SPQ ID NO: 16099.  
XX Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
XX EPI033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
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PR 31-AUG-1999; 99US-0151438.  
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PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 9.3%; Score 83.6; DB 21; Length 683;  
Best Local Similarity 52.7%; Pred. No. 0.00032;  
Matches 232; Conservative 0; Mismatches 199; Indels 9; Gaps 2;

QY 255 GCGAGGGGAGGAGTACTGGCGCCGACACACAGGGCGCGCGTGGCGTGGCC 314  
DB 204 GCAGCAGCTTAAGCTTACCGAGTGCACAAACGCGCAAGTCAGTGGTTCACA 263  
QY 315 CCGCTGCGGTGGAACGCGCGCTTCGGCGCGCGCGGAGCGTGGCGCCACAGCGG 374  
DB 264 CCACTAGTTTGGAGCCAGACCTTGGAAAGCTCTCGAGTGCCTTCCGTTACCAAGG 323  
QY 375 CGGAGGGCGGCGCTTCGGCGAGCTGGGGCCAGCCCTTACGGCGGACCAAGG 434  
DB 324 AACCAAAAGAGTGTGAGTTCGCGAGTCAACCTGGAATAATACGGCGGCAACACACTT 383  
QY 435 TGGGAGACTACG-----CGGCGCGCGCGCGAGGTGGCGGTGGGTGGCGAG 488  
DB 384 TGGGCTAAGGCTTATGATGCGGTACACCGTCTTCTGTGGAGCTTGGGTAAAGAG 443  
QY 489 GGGCGGTATACACCCACGACACACAGTGGCGCGCGGGGCGAGTGGCGACGTAC 548  
DB 444 AAACCTTTCTACATTTATAGTCAAGACACGTGTCTCGCAACCAACACGTGCGGGTTAT 503

QY 549 ACGCAGTGTGTGGCGACACCGCGAGGTGGCGCGAGCGCCAGCTGGCCAGC 608  
DB 504 AAACAGTGTGTGGAGAACTTAAGAGCTCGGGTGTCTAAGCGACGTGACGAAA 563  
QY 609 GGGCGCC--GCTCAGCGCTTGCCTGTACAAACCGACGCGACACGTGACGAGC 665  
DB 564 GAGTCAACGTTGTGACCATTTGTTTTACATCTCTCTGSAATATATATGGCCAAA 623  
QY 666 CCGTACTAGCTAGCTGAGCT 685  
DB 624 CCTTACTAGCAAAATTGGAT 643

RESULT 10  
AAK53491/c  
ID AAK53491 standard; DNA; 114955 BP.  
XX  
AC AAK53491;  
XX  
DT 05-JUL-1999 (first entry)  
XX  
DE Human adenosine A1 receptor antisense oligonucleotide fragment.  
XX  
KW Antisense oligonucleotide; multiple target; antisense treatment;  
KW impaired respiration; inflammation; lung disease;  
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;  
KW acute asthma; allergy; asthma; impeded respiration;  
KW respiratory distress syndrome; pain; cystic fibrosis;  
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;  
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
KW prostate cancer; ss.  
XX  
OS Synthetic.  
XX  
PN WO9913886-A1.  
XX  
PD 25-MAR-1999.  
XX  
PE 17-SEP-1998; 98WO-US19419.  
XX  
PR 09-JUN-1998; 98US-0093972.  
PR 17-SEP-1997; 97US-0059160.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
XX WPI; 1999-229400/19.  
XX  
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary  
PT vasoconstriction  
XX  
PS Disclosure; Page 37; 120pp; English.  
XX  
XX

The specification describes antisense oligonucleotides (AAK52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAK5272-74. These multiple target oligonucleotides (specifically AAK5180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,

|        |  |
|--------|--|
| KM     | hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis; |
| XX     |  |
| XX     | prostate cancer; ss.   |
| OS     |  |
| XX     | Synthetic.   |
| XXXXXX |  |

XX

XX

XX

PR 17-SEP-1997; 97US-0059160.

PA (UYEC-) UNIV EAST CAROLINA.

PI NYce JW;

DR WPI; 1999-229400/19.

PT New antisense oligonucleotides used in treatment of, e.g. pulmonary  
 PM metastatic disease

XX Page 37: 120ms: English

the specific antisense oligonucleotides (AAX52869-X55271).

CC directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene

CC Initiation codons, genomic flanking regions, intron-exon borders, the  
5'-end, the 3'-end and the juxta-section between coding and non-coding  
CC

CC regions and all segments of RNAs encoding proteins associated with one  
CC or more diseases, conditions or mixtures. The antisense oligonucleotides

may be derived from sequences AA552/2-74. These multiple copies of nucleotides (specifically AA55180-271) can be used for the

conditions are those associated with impaired respiration and

CC Inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded  
CC inflammation, infectious diseases, pulmonary tuberculosis,  
CC inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded

CC respiratory distress syndrome, pain, cyanosis, tachypnea, tachycardia, hypoxemia, hypercapnia, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic

CC Lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,

hepatic metastases, as well as all types of cancers which may metastasize

[illegible][illegible]

Best Local Similarity 34.28; Pred. No. 0.00051;

[illegible]

10470

[illegible]

10484

300

10490

350

10405

413

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473









DB 4334 ACGGGGGGAGAGCGGGGGGCTCCCGGGCCCGGGCCCGGGCGGCTCGGAGCG 4393  
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 QY 564 CGCAACACGGCGAGGTGGGGTGGCGGACGCGACGTCGCGGCGGCG 609  
 DB 4454 CGGGCGGGGGCCCGCTCAGCGCTGTAGCGCACACGCGGCGCCACGG 4499

## RESULT 15

ABQ40858

ID ABQ40858 strand: DNA; 712 BP.

AC ABQ40858;

DT 12-JUL-2002 (first entry)

XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 27449.

XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
 KW drug; side effect; cancer; central nervous system; cardiovascular;  
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
 KW SNP; cell differentiation; ds.

XX Homo sapiens.

PN WO200218632-A2.

PD 07-MAR-2002.

PF 01-SEP-2001; 2001WO-BP10074.

PR 01-SEP-2000; 2000DE-1043826.

PR 05-SEP-2000; 2000DE-1044543.

XX (EPIC-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K, Guetig D;

XX WPI; 2002-371829/40.

PT Determining the degree of cytosine methylation in genomic DNA, useful  
 PT for diagnosis and prognosis, comprises selective hybridization of  
 PT amplicons from chemically treated DNA

PS Claim 12; 56pp + Sequence Listing; 56pp; German.

CC This invention describes a novel method for determining the degree of  
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
 CC genomic sample of DNA. The sample is treated chemically to convert  
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
 CC DNA that contains the target C is amplified to form a labeled amplicon.  
 CC The amplicon is hybridised to two classes, each with at least one  
 CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers  
 CC and the degree of hybridisation to both classes is determined from the  
 CC label on the amplicon. From the ratio of labels hybridised to the two  
 CC classes of oligomers, the degree of methylation is calculated. The method  
 CC is used: (i) for diagnosis and/or prognosis of side effects of  
 CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders  
 CC of the central nervous, cardiovascular, gastrointestinal and respiratory  
 CC systems etc., particularly by detecting mutations or single nucleotide  
 CC polymorphisms (SNP/s); and (ii) for differentiation of cell or tissue  
 CC types and for investigating cell differentiation. The method allows the  
 CC methylation status of many C residues to be determined simultaneously.  
 CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the  
 CC method for determining the degree of cytosine methylation described in  
 CC the disclosure of the invention.

XX Sequence 712 BP; 12 A; 181 C; 456 G; 47 T; 16 other;

Query Match 7.8%; Score 70; DB 24; Length 712;  
 Best Local Similarity 47.1%; Pred. No. 0.034;  
 Matches 226; Conservative 0; Mismatches 252; Indels 2; Gaps 1;

QY 147 GCGCTCTGCGCCCGCGCGCGCGGACCCAGCGGGCGCGGCTCTCATTTGCGGGGCGCGCG 206  
 DB 231 GGGCGCGCGCGGTCGGGGCGGGCGGGCGGCTTCGCGGTCGGGGCGGGCGGGCGGGCG 290  
 QY 207 GCGCGGTGACCAAGAGCGCAGCAGGTGACACCGGCGGCGGCGGCGGCGGCGGCGGCG 266  
 DB 291 TCGCGGGGCGCGCGCGGGGGGGGTTTCGCGGCGCGCGGGGGGGGGGTTTCGCGCGCG 350  
 QY 267 GAGTACCTGCGCGCGCAACAAGCGCGCGCGCGCGCGGTGGCCCGCGCGCGGTGG 326  
 DB 351 GGTGCGGGGGGGGGTTCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 410  
 QY 327 AACGCGGGCGCTGGGCTTCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 386  
 DB 411 NGCGGGCGGGCGGTTTCGGGGCGGGGGCGGAGGGCGGGCGGAGCGGCGGCGGCGGCG 468  
 QY 387 TCGCGCTTTCGCGACGTGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 446  
 DB 469 CGCGGGCGGGGGGTCGGGGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 528  
 QY 447 CGCGCGCGCGCGCGCGGAGGTGTGCGCTGTGGGTGGCGGAGGGGGGTACTACACCGAC 506  
 DB 529 NGCGGGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 588  
 QY 507 GCCAACACACAGTGTGCGCGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 566  
 DB 589 GAGCGCGGTTCGCGCGCGCGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 648  
 QY 567 AACACCGCGGAGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 626  
 DB 649 GGTGCGGGGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 708

Search completed: March 18, 2003, 14:12:18  
 Job time : 374 secs